

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 04:09:48 ; Search time 2080 Seconds  
(without alignments)  
3425.968 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgcgcgcgcgcgcgccttc.....ggaatntagataaaaaaant 440

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

BST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	267.6	60.6	974	11	AY108359	Zea mays
2	266.6	60.6	492	10	AW424591	AW424591 707018G10
3	258.6	58.8	646	14	BO487045	BO487045 1091050G1
4	246.6	56.0	491	9	A1948185	A1948185 603037E02
5	225.2	51.2	583	10	BE553166	BE553166 945089H09
6	222.8	50.6	511	13	BI233723	BI233723 945032B03

7	218	49.5	531	10	AW925193	AW925193 WSL_76_E1
8	217.4	49.4	508	10	BE552951	BE552951 946087G06
9	217.2	49.4	991	11	AY104688	AY104688 Zea mays
10	169.2	38.5	243	10	BE511251	BE511251 946059A03
11	127.2	28.9	450	9	AL822592	AL822592 AL822592
12	126.6	28.8	453	17	BH217843	BH217843 1005060C1
13	126.4	28.7	603	10	BE404891	BE404891 WHE1206_D
14	126.4	28.7	791	14	BQ483893	BQ483893 WHE3513_G
15	125	28.4	1206	10	BE421015	BE421015 HWM004_HO
16	124.8	28.4	460	12	BG904016	BG904016 TaLR1110B
17	124.8	28.4	486	10	BE499155	BE499155 WHE0970_F
18	124.8	28.4	500	10	BE405417	BE405417 WHE1216_B
19	124.8	28.4	535	12	BG904017	BG904017 TaLR1110B
20	124.8	28.4	571	13	BG909866	BG909866 TaLR1110A
21	124.8	28.4	571	13	BM134936	BM134936 WHE0460_A
22	124.8	28.4	596	10	BE500781	BE500781 WHE0991-0
23	124.8	28.4	733	14	BO579753	BO579753 WHE2974_B
24	124.2	28.2	557	13	BM375207	BM375207 EBem06_SO
25	123.6	28.1	473	13	BI778921	BI778921 EBem01_SO
26	123.6	28.1	578	14	BQ759854	BQ759854 EBP105_SO
27	123.6	28.1	601	14	BQ767075	BQ767075 EBR008_SO
28	123.6	28.1	608	14	BQ765728	BQ765728 EBR003_SO
29	123.6	28.1	621	13	BM370509	BM370509 EBR008_SO
30	123.6	28.1	636	12	BF625593	BF625593 HYSMEA001
31	123.6	28.1	650	13	BI958490	BI958490 HYSMEH001
32	123.6	28.1	655	13	BI778583	BI778583 EBR007_SO
33	123.6	28.1	800	12	BG299552	BG299552 HYSMEC002
34	123.6	28.1	865	12	BF620735	BF620735 HYSMEC002
35	123.6	28.1	879	13	BI949512	BI949512 HYSME1001
36	123.4	28.0	992	10	BE040565	BE040565 OF03B04_O
37	123.2	28.0	411	9	AL828336	AL828336 AL828336
38	123.2	28.0	539	9	AL825800	AL825800 AL825800
39	123.2	28.0	554	12	BG262856	BG262856 WHE0948_B
40	122.6	27.9	568	9	AL504667	AL504667 AL504667
41	122.4	27.8	359	14	BQ606346	BQ606346 BRL_2201
42	122.4	27.8	577	12	BF474747	BF474747 WHE2105_F
43	121.8	27.7	445	9	AUI72608	AUI72608 AUI72608
44	121.6	27.6	431	12	BG314081	BG314081 WHE2467_H
45	121.6	27.6	475	12	BG312596	BG312596 WHE2455_F

#### ALIGNMENTS

RESULT 1						
AY108359						
LOCUS	AY108359	974 bp	mrna	linear	HTC 25-MAY-2002	
DEFINITION	Zea mays PC0061446 mRNA sequence.					
ACCESSION	AY108359					
VERSION	AY108359.1					GI:21211437
KEYWORDS	HTC					
SOURCE	Zea mays.					
ORGANISM	Zea mays					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.					
AUTHORS	Haines C.F., Dolan M., Miao G.H., Vogel, J.M., Whitsitt, M.S., Arthur L.W., Hanafey M., Morgante M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 974)					
AUTHORS	Coe, E.C.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002)					
FEATURES	Missouri, Columbia, MO 65211, USA					
source	1. .974					
	/organism="Zea mays"					
	/db_xref="MaizeDB:633254"					
	/db_xref="taxon:4577"					
	/clone="PC0061446"					



<div><div>JOURNAL COMMENT</div><div>Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 1091050 row: G column: 11. Location/Qualifiers</div></div>	<div><div>FEATURES source</div><div>1..646 /organism="Zea mays" /cultivar="OH43" /db_xref="taxon:4577" /clone_lib="1091 - Immature ear with common ESTs screened by Schmidt lab" /tissue_type="Inflorescence meristem - floral organ primordia" /dev_stage="0.5 cm to 2 cm" /lab_host="Stratagene XL0LR" /note="Organ: Immature ear; Vector: pAD-GAL4; Site_1: EcoRI; Site_2: XhoI; RNA from library 606 was filtered for common ESTs found in 506." BASE COUNT 130 a 165 c 198 g 153 t ORIGIN</div></div>	<div><div>Query Match 58.8%; Score 258.6; DB 14; Length 646; Best Local Similarity 77.5%; Pred. No. 1e-58; Matches 334; Conservative 0; Mismatches 91; Indels 6; Gaps 4;</div><div>QY 10 CGCGCGCTTCGCTTCGTCGCCGCTCAGCGTCCGCGCTCCGCTCGCGCTC 69 DB 1 CGCGCGACCGCGCTTCGTCGCCGCTCAGCGTCCGCGCTCCGCTCGCGCTC 60 QY 70 ACCGGCGGAGGAGGCGAGCGGTGCGCGATGCGGTGCGGTGCGGTGCGGTGCGG 129 DB 61 ACCGGCGGAGGAGGCGAGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGG 120 QY 130 GNGATCGNCTTCATCCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGAG 189 DB 121 GGGATCGCTTCCTCCATCGCGGTGATCCCGCTTCGCGTTCGCGTTCGCGTTCGAG 180 QY 190 GACATCANGANGTGTGTCGATCCCAAGCGGTCCGTCGACACATATACCATTTTGTCT 249 DB 181 GACATCAGCAGCTTGTGCTCGATCCCAAGCGGTTCGCTGACACATTCGACCTTTGTCT 240 QY 250 AAGCGGTACAGGACACAGGATACACCTGGAATAGAGTTAAAGCTAGAGGATCA 309 DB 241 GAGCGGTACAGGACACAGGATACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299 QY 310 TTTCGGAACAACCTANNCTTANANAATTTGGTCAAAATTTGGTGCNATTTGAGGAAC 369 DB 300 TTTCGCTTCCTTCATCGCTT--TAGCCATTGGCGCAAAATTTGCT--TTGAGGAAGCC 356 QY 370 NAAATNAGTCCGANGCAAAATGATTTTNGAATANGAATTTTNGGAATNNGGAATNTTA 429 DB 357 GAAGAAGTTGCCAGGCGAGGTGATCT--CCGAAGAGTATTCTTTGGAATATGGAATGAC 414 QY 430 GATAAAAAAT 440 DB 415 AAGATAGAAAT 425</div></div>	<div><div>RESULT 4 AT948185 LOCUS AT948185 491 bp mRNA linear EST 19-AUG-1999 DEFINITION 603037E02.x1 603 - stressed root cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence. ACCESSION AT948185 VERSION AT948185.1 GI:5740495 KEYWORDS Zea mays. SOURCE Zea mays. ORGANISM Zea mays.</div></div>
<div><div>JOURNAL COMMENT</div><div>Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 1091050 row: G column: 11. Location/Qualifiers</div></div>	<div><div>FEATURES source</div><div>1..491 /organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone_lib="603 - stressed root cDNA library from Wang/Bohnert lab" /tissue_type="seedling" /dev_stage="salt stress" /lab_host="E. coli XL Gold" /note="Organ: root; Vector: pBluescriptII SK(+); XR: Seedling stressed root cDNA library from Wang/Bohnert lab" BASE COUNT 76 a 165 c 148 g 100 t 2 others ORIGIN</div></div>	<div><div>Query Match 56.08; Score 246.6; DB 9; Length 491; Best Local Similarity 83.6%; Pred. No. 1.5e-55; Matches 275; Conservative 0; Mismatches 53; Indels 1; Gaps 1;</div><div>QY 1 CGTCCGCGCGCGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTGAGC 60 DB 163 CGTCCGCGCGCGCGCGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTGAGC 222 QY 61 GTGCGGCTCACCGCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 120 DB 223 GTGCGGTTCACCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 282 QY 121 CGTTCGCGGATCGCTTCCTTCATCCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT 180 DB 283 CGCTTCGCGGAGTGCCTTCCTCATCGCTTCCTCATCGCTTCCTCATCGCTTCCTCATCGCT 342 QY 181 ATGTTTCAGGATCANGANGTGTTCGATCCCAAGCGGTTCGATCCCAAGCGGTTCGATCCCAAGCGGT 240 DB 343 ATGTTTCAGGATCANGANGTGTTCGATCCCAAGCGGTTCGATCCCAAGCGGTTCGATCCCAAGCGGT 402 QY 241 CATTTTGTCAAGCGGTCAAGGACCAAGGATACACCTTCACCTTCACCTTCACCTTCACCTTCACCT 300 DB 403 CTCTTTGTCCAGCGGTACAGGACCAAGGATACACCTTCACCTTCACCTTCACCTTCACCTTCACCT 461 QY 301 AGGTTTCATTTTCGGAACAACCTANNCTTT 329 DB 462 AGGTTTCATTTTCGTTCTCTCTATCGCTT 490</div></div>	<div><div>RESULT 5 BE553166 LOCUS BE553166 583 bp mRNA linear EST 10-AUG-2000 DEFINITION 946089H09.y1 946 - tassal primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence. ACCESSION BE553166 VERSION BE553166.1 GI:9794858 KEYWORDS Zea mays. SOURCE Zea mays. ORGANISM Zea mays.</div></div>

REFERENCE 1 (bases 1 to 583)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
UNIVERSITY University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu  
Plate: 946089 row: H column: 09.  
LOCATION/Qualifiers  
1. .583  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="946 - tassels primordium prepared by Schmidt lab"  
/tissue\_type="tassels"  
/dev\_stage="just after the transition from vegetative to inflorescence development"  
/lab\_host="X10LR"  
/note="Organ: tassels; Vector: HybridZAP; Site.1: EcoRI; Site.2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 kb average."  
BASE COUNT 114 a 157 c 175 g 137 t  
ORIGIN  
Query Match 51.28; Score 225.2; DB 10; Length 583;  
Best Local Similarity 73.48; Pred No. 9e-50;  
Matches 309; Conservative 0; Mismatches 106; Indels 6; Gaps 4;  
QY 20 CGCCTTTTCGCCCGCTCAGCGTCGCGGCTCCNNAGCGTCCGCGTACCGCGGCA 79  
DB 6 CGCCTTTTCGCCCGCTCAGCGTCCGCGCTCCACTGGCGTCCGCGTACCGCGGGA 65  
QY 80 GCGGAGGCGGCGGTGGTGGCGATGGCGTTCGCTGATCCGCGTTCGGCGNGATCGNCT 139  
DB 66 GCGGAGGCGGCGGTGGTTCGCGATGGCGTTCGCGGAGCGCTCGCTTGGCGGGGTTCCT 125  
QY 140 CTTNATCCNGGNTATNCCGACCTTCCAAAGCCAGGATNATGTTTCAGGACATCANGA 199  
DB 126 CTTCCATCCGCGTATCCCGGCTTTCCCAAGCCAGGTATTTTCTCCAGGACATCAGA 185  
QY 200 NGTNGTGTTCGATCCCAAGCGGNTCCGTGACACATATACCATTTGTCAAGCGGTACA 259  
DB 186 CACTGCTGCTCGACCCCAAGCGGTTCGCGTACCATCGACTCTTCGTTGAGCGGTACA 245  
QY 260 AGGACCAAGGATACACCTTGGAAATAGGAGTTAAAGCTAGAGGNTCANTTTCGGAACA 319  
DB 246 AGGACCAAGGATACACCTGAGTTGCT-GGTGTGGAAGCTAGAGGTTTCATTTTGGTCTC 304  
QY 320 ACTANNTCTTANAANNAATGTGTAATAATNGTGNCAATTCAGCAAGCNAATNAGTGT 379  
DB 305 CTTATCGCT--CTAGCATCGTGCTAAATTTGT-ACCTTTTGAAGGAGCGAAGTTG 361  
QY 380 CCANGCNAATGATTTTNGAANAATGAAATTTTNGAATNNGAATNNTAGATAAANAAN 439  
DB 362 CCAGCGGAGGTGATCT--CCGAGAATATTTCTCTGGATACGGAATGACAGATAGAGA 419  
QY 440 T 440  
DB 420 T 420

RESULT 6  
BI233723  
LOCUS BI233723  
DEFINITION 949032B03.y2 949 - Juvenile leaf and shoot cDNA from Steve Moose

ACCESSION BI233723  
VERSION BI233723.1 GI:14701305  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
REFERENCE 1 (bases 1 to 511)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 949032 row: B column: 03.  
LOCATION/Qualifiers  
1. .511  
/organism="Zea mays"  
/cultivar="M64A"  
/db\_xref="taxon:4577"  
/clone\_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"  
/tissue\_type="immature leaf primordium and vegetative meristem"  
/dev\_stage="4 stages from 3-13 days after imbibing"  
/lab\_host="E. coli X10LR"  
/note="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site.1: EcoRI; Site.2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled: polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybridzap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil; 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5; primordia from 6-8, and the vegetative apex; 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing; 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT 105 a 130 c 156 g 120 t  
ORIGIN

Query Match 50.68; Score 222.8; DB 13; Length 511;  
Best Local Similarity 76.28; Pred No. 3.7e-49;  
Matches 308; Conservative 0; Mismatches 89; Indels 7; Gaps 5;  
QY 37 GTCAGGCTCGCGGCTCCNNAGCGTCCGCGTACCGCGGCGGAGGCGAGCGCGGTG 96  
DB 1 GTCAGGCTCGCGGCTCCGACTG-CGCTGCGGTGTCACGCGGCGGAGGCGAGCGCGGTG 59  
QY 97 GTGGCGATGCGCTNCGCTGATGCGCGCTTCGGCGNGATCGNCTTCATCCNGGTNATN 156  
DB 60 GTGGCGATGCGCTCGCGGTGAGCGCGCTTCGGCGGATCGCGCTCCCTCCATCGCGTCA 119  
QY 157 CCGGACTTCCAAAGCCAGGAGTATGTTTTCAGGACATCANGANGTNGTGTTCGATCCC 216  
DB 120 CCGGACTTCCCAAGCCAGGAGTATGTTTTCAGGACATCAGGAGTGTGCTGCTCATCC 179  
QY 217 AAGCGGNTCCGTGACACATATACCATTTTGTCAAGCGGTACAGGACCAAGGATCACC 276  
DB 180 AAGCGGNTCCGTGACACATATACCATTTTGTGAGCGGTACAGGACCAAGGATCACC 239  
QY 277 NTGGAANTAGGAGTTAAAGCTAGAGGNTCANTTTCGGAACAACATANNCTTTANAANA 336  
DB 240 GTGGTTGCT-GGTGTTGAAGCTAGAGGTTTCATTTTGGTCTCTCTCGCTT--TAGCC 296





```

QY 143 NCATCCGCTNATCCGCACTTCCCAAGCCAGGATNATGTTTTCAGGACATCANGANGN 202
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 CCATCCGCGTATCCCGCACTTCCCAAGCCAGGATCATGTTTCAGGACATCAGCAC 182

QY 203 TGWGTTCATCCCAAGCGNCCGTGACACATATACCATTTTTCAGCGGTACAAAG 262
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183 TGCTGCTCACCACCAAGCGGTTCCGTGACACCATCGACCTTCGTTGAGCGGTACAAAG 242

QY 263 ACCAAGNATACCCNTGGAANTAGGAGTTAAAGCTAGAGGNTCANTTTTCGGACAACT 322
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 ACCAAGGATACCGGTAGTTGCT-GGTGTGGAAGCTAGAGGGTTTCATTTTGGTCCCTCT 301

QY 323 ANNTCTTANAANNAATGGTCAAAAAATGGTGNATTTNGGAATNGGAATNNTAGATAAAAAANT 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 ATGCT--CTAGCCATCGGTAAATTTGT-ACCTTTGAGGAAGCCGGAAGAGTTGCCA 358

QY 363 NGCNAATGATTTTANCAATANCAATTTTNGGAATNGGAATNNTAGATAAAAAANT 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 GCCGAGGTATCT--CCGACATATCTCTCGATACCGNACTGACAGATAGAGAT 414

RESULT 9
AY104688
LOCUS AY104688 991 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC0061445 mRNA sequence.
ACCESSION AY104688
VERSION AY104688.1 GI:21207766
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays
REFERENCE 1. (bases 1 to 991)
AUTHORS Rainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2. (bases 1 to 991)
AUTHORS Coc,E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES
    source
        1..991
            /organism="Zea mays"
            /db_xref="MaizeDB:633253"
            /db_xref="taxon:4577"
            /clone="PC006145"
            /clone_lib="Maize Mapping Project/DuPont Consensus
            Library"
            /note="this sequence is part of a project of EST
            assemblies resulting from the application of public
            contigs to seed DuPont contigs; this resource was
            assembled by DuPont as part of a collaboration for the
            overgo addressing of BACs in conjunction with the Maize
            Mapping Project"
BASE COUNT 242 a 240 c 263 g 246 t
ORIGIN
Query Match 49.4%; Score 217.4; DB 11; Length 991;
Best Local Similarity 72.4%; Pred. NO. 1.4e-47;
Matches 31; Conservative 0; Mismatches 114; Indels 7; Gaps 5;

QY 4 CCGCGCGCGCGCACTTCGCTTTTCGCCCGCGTACAGCTCGCGGCTCCNNTGAGCGT- 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 CCGTCCGCGTCCGCGCGCGCTTTTCGCCCGCGTTCGCGTTCGCGTCCACTGGCGGTG 126

QY 63 GCGCGTCCACCGCGCGAGCGAGCGAGCGGTGGTGGCGATGCGGTNGCGTATGCGCG 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 GCGCGTCCACCGCGGAGCGAGCGAGCGGTGGTGGCGATGCGGTTCGCGTCCCGCGCGCGCG 186

```

```

QY 123 CTTGGCGGNGATCGNCTCTTCATCCNGGTNATNCCCGACTTTCNCCAAAGCCAGGATNAT 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 CTTGGCGGNGATCGNCTCTTCATCCNGGTNATNCCCGACTTTCNCCAAAGCCAGGATNAT 246

QY 183 GTTTCAGGACATCANGANGNTGTTGTCATCCCAAGCGNCCGTGACACATATATACCA 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 GTTTCAGGACATCAGACACTGCTGCTGACCCCAAGCGCTTCGCTGACACCATCGACCT 306

QY 243 TTTTGTCAAGCGGTACAGGACCAAGNATCNCNTGGAANTAGGAGTTTAAAGCTTAGAG 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 CTTGCGTTCAGCGGTACAGGACCAAGGATCNCCTGAGTGTCT--GGTGTGAAGCTTAAG 365

QY 303 GGNTCANTTTTCGGAACCAACTTANNCTTANAANNAATTTGTCAAAATNGTGNCAATTTCA 362
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 GGTTCATTTTGGTCCCTCTATGCT--CTAGCATCGGTGCTAAATTTGT-ACCTTTTCA 422

QY 363 GGAAGCNAATNAGTCCANGCNAATGATTTTNGAATANGAATTTTNGGAATNNGG 422
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 423 GGAAGCNAATNAGTCCANGCNAATGATTTTNGAATANGAATTTTNGGAATNNGG 480

QY 423 AATNTAGATAAAAAANT 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 AACTGACATAGATAGAT 498

RESULT 10
BE511251
LOCUS BE511251 243 bp mRNA linear EST 07-AUG-2000
DEFINITION 946059A03.y1 946 - tassels primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION BE511251
VERSION BE511251.1 GI:9732499
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
REFERENCE 1. (bases 1 to 243)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946059 row: A column: 03.
FEATURES
    source
        1..243
            /organism="Zea mays"
            /cultivar="OH43"
            /db_xref="taxon:4577"
            /clone_lib="946 - tassels primordium prepared by Schmidt
            lab"
            /tissue_type="tassels"
            /dev_stage="just after the transition from vegetative to
            inflorescence development"
            /lab_host="XL0LR"
            /note="Organ: tassels; Vector: HybridAP; Site 1: EcoRI;
            Site 2: XhoI; George Chuck dissected immature tassels
            between 1mm and 3mm. Sharon stanfield prepared the cDNA
            library in HybridAP. Sample insert size range was 350 bp
            to 3 Kb with a 1 Kb average."
BASE COUNT 29 a 93 c 74 g 47 t
ORIGIN
Query Match 38.5%; Score 169.2; DB 10; Length 243;
Best Local Similarity 81.4%; Pred. NO. 6.5e-35;

```

Qy	219	GGGNTCCGTGACACATATACCATTTTGCACGCGGTACAAGCACCAGGHNATCCACNT	278
Db	250	GGCATTTCCGTGACACCACTGACCTCTTTTGCAGCGGTACAAGCAACAAGACATAACTGT	309
Qy	279	GGAAATAGGAGTTAAAGCTAGAGGNTCANTTTCGGAACAACATANNCTTTANAANNAAT	338
Db	310	AGTTACT-GGTGTGTAAGCCAGAGATTCATTTTTTGGTCTCCCATTCG--ATTAGGCAT	366
Qy	339	TGGTCAAAAATNGGTGNCNATTTGAGGAAGCNAAATNAGNTGCCAAGCNAAATGATTT	395
Db	367	AGGTGCAAGTTTGTG-TCCAAATAAGGAAGCCGAATAATTTACCTGGTGAGGTGATAT	422

RESULT 12  
BH217843  
LOCUS  
DEFINITION  
BH217843 453 bp DNA linear GSS 08-NOV-2001  
1006060C11.y1 1006 - Rescuemu Gr1d Zea mays genomic, DNA  
sequence.

ORGANISM	zea may
Eukaryota:	
Viridiplantae:	Streptophyta; Tracheophyta;
Spermatophyta:	Magnoliophyta; liliopsida; poales; PACC
Clade:	Panicoidae; Andropogoneae; zea.
REFERENCE	1. (bases 1 to 453)
WALBOT-V	
ARMHOF	

Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site found so sequence was trimmed.  
Post-ligation sequence submitted separately.  
Submitted to Genbank on 11/05/00

```

/c/one_lib="100b - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"

/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site.1: BamHI; Site.2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmmbd.iastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with

```

Site [www.zmboi.lustat.edu](http://www.zmboi.lustat.edu) and follow the links for "RescueMu." Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BanHI and BglII, and ligated to form circular plasmids. D10B cells were transformed and then screened on LB plates with ampicillin.

[illegible]

```

QY 70 ACCGGCGGAGGCGAGGCGGTGGCGATGCGTNCGCTGATCGCGCTGGG 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 ACCGGCGGAGGCGAGGCGGCGGTGGCGATGCGTNCGCTGATCGCGCTGGG 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130 GNGATGCTCTCATCCGCTGATCCGCGTTCATCCGCGTTCATCCGCGTTC 176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 GGGATGCTCTCATCCGCGTTCATCCGCGTTCATCCGCGTTCATCCGCGTTC 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
BE404891 603 bp mRNA linear EST 21-JUL-2000
LOCUS WHE1206_D01_G02s Wheat etiolated seedling root cDNA library
DEFINITION Triticum aestivum cDNA clone WHE1206_D01_G02, mRNA sequence.
ACCESSION BE404891
VERSION BE404891.1 GI:9364359
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
          ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 603)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
          ,P.S., Hsiao,C.C., Kang,J.C., Lazo,G.R., Miller,R., Rausch,C.J.,
          Seaton,C.L. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat
          genomes
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
          US Department of Agriculture, Agriculture Research Service, Pacific
          West Area, Western Regional Research Center
          800 Buchanan Street, Albany, CA 94710, USA
          Tel: 5105595773
          Fax: 5105595818
          Email: oanderson@pw.usda.gov
          Sequences have been trimmed to remove vector sequence and low
          quality sequence with phred score less than 20
          Seq primer: Strategene SK primer.
          Location/Qualifiers
            1..603
              /organism="Triticum aestivum"
              /cultivar="Chinese Spring"
              /db_xref="taxon:4565"
              /clone="WHE1206_D01_G02"
              /clone_lib="Wheat etiolated seedling root cDNA library"
              /tissue_type="Root"
              /dev_stage="Five day old etiolated seedling"
              /lab_host="E. coli SOLR"
              /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
              Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
              , germinated and grown aseptically in the dark at room
              temperature on filter paper with water, nystatin and
              cefotaxime in covered crystallization dishes. Roots were
              harvested. The tissue, total RNA, and poly(A) RNA were
              prepared. A cDNA library was made, and the cDNA clones
              were in vivo excised to give phagescript phagemids in the
              TJ Close lab (Choi, Close, Fenton) at the University of
              California, Riverside. Plasmid DNA preparations and DNA
              sequencing, were performed in the OD Anderson lab (all
              other authors)."
BASE COUNT 131 a 153 c 182 g 137 t
ORIGIN

Query Match 28.7%; Score 126.4; DB 10; Length 603;
Best Local Similarity 65.3%; Pred. No. 2.7e-23;
Matches 233; Conservative 0; Mismatches 116; Indels 8; Gaps 5;

QY 39 CAGCGTCGCGGCTCCNTTGGCTGCGTCCACCGCGGCGGCGAGGCGCGGTGGT 98
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 CTGCGGTTGCGATCCCGGAGGCGGTGCGGCTTCGGC-GCGGCGAGGCGGTGG 89
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 99 GCGGATGCTGCTGATCGCGCTGGCGGNGATCGCTCTCATCCGCGTTCATCC 158
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Db 90 CGCGATGGCATCC---GACGGGCGGTGGAGCGGATCGCTCCAGCATCCGCGCATCC 146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 159 CGACTTNCACAAAGGCGAGGATGTTTTCAGGACATCANGANTGTTGTTTCGATCCAA 218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 CAACCTTCCCCAAGCGAGGATTTTGTTCAGGACATCACAACTTCTCTCGATCGCA 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 219 GCGGTCGCTGACACATATACCATTTTGTCAAGCGGTACAGGACCAAGGATACACCT 278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 GCGATTCGCTGACACCTGACCTCTTTGTGCGGCGGTACAGGACCAAGACATCACTGT 266
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 279 GGAATATAGAGTTTAACTAGAGGNTCANTTTCGGAACAACCTANNCTTTANNAAT 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 ACTTGCT-GGTGTGAAGCCAGAGGATTCATTTTGGTCTCCCATTCG--ATTAGCCAT 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 339 TGGTCAAAATNGTGNCATTTAGGAAGCANNATNAGTGCAGCAGCANNATGATTT 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 AGGTGCAAGTTTGT-TCCAAATAGGAAGCCAAAAAATTACCTGTGAGGTGATAT 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
BQ483893 791 bp mRNA linear EST 03-JUN-2002
LOCUS WHE3513_G10_M19s Wheat unstressed root cDNA library Triticum
DEFINITION aestivum cDNA clone WHE3513_G10_M19, mRNA sequence.
ACCESSION BQ483893
VERSION BQ483893.1 GI:21319829
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
          ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 791)
AUTHORS Anderson,O.D., Chao,S., Close,T.J., Crossman,C., Fenton,R.D., Lazo
          ,G.R., Nguyen,H.T., Rausch,C.J., Wilson,C.J., Woo,J. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat
          genomes Unstressed root cDNA library
JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
          US Department of Agriculture, Agriculture Research Service, Pacific
          West Area, Western Regional Research Center
          800 Buchanan Street, Albany, CA 94710, USA
          Tel: 5105595773
          Fax: 5105595818
          Email: oanderson@pw.usda.gov
          Sequences have been trimmed to remove vector sequence and low
          quality sequence with phred score less than 20
          Seq primer: SK primer.
          Location/Qualifiers
            1..791
              /organism="Triticum aestivum"
              /cultivar="Chinese Spring"
              /db_xref="taxon:4565"
              /clone="WHE3513_G10_M19"
              /clone_lib="Wheat unstressed root cDNA library"
              /tissue_type="Roots"
              /dev_stage="Full tillering"
              /lab_host="E. coli SOLR"
              /note="Vector: Lambda Uni-ZAP XR, excised phagemid
              phagescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants
              were grown until full tillering stage and root tissue was
              collected at Texas Tech University (Zhang, Ht Nguyen Lab
              ). Total RNA and poly(A) RNA were prepared, a cDNA
              library was made, and the cDNA clones were in vivo
              excised to give phagescript SK(-) phagemids in the TJ
              Close lab (Close, Fenton) at the University of California
              , Riverside. Colony plating, plasmid DNA preparations
              and DNA sequencing were performed in the OD Anderson lab
              (all other authors)."
BASE COUNT 171 a 215 c 222 g 183 t
ORIGIN

```

Query Match 28.7%; Score 126.4; DB 14; Length 791;  
 Best Local Similarity 65.3%; Pred. No. 3e-23;  
 Matches 233; Conservative 0; Mismatches 116; Indels 8; Gaps 5;

Qy 39 CAGCGCTCGGCTCCNNMTGAGCGTGCACGGCGCGCAGGCGAGGCGCGGTGGT 98  
 Db 104 CTGCGGTTCCGATCCCGCGAGGCGTCCGCTTCGCGC-GCGGGCGAGGGTCGCGCGGT 162

Qy 99 GCGAGTGGCTGCTGATGCGCGCTTGGCGGNGATCGCTTCGATCCGCTTCGATCC 158  
 Db 163 CCGGATGGCATCC---GAGCGGCGGCTGGAGCGGATCCGCTTCGATCCGCGCATCC 219

Qy 159 CGACTTCCAAAGCAGGATNATGTTTCAGGACATGANGANGTGTGTCATCCCAA 218  
 Db 220 CAACCTTCCCAAGCAGGATTTGTTAGGACATCAACCTTGTCTCGATCCGCA 279

Qy 219 GCGGTTGCGTCAACATATACCATTTTTCGAGCGGTACAGGCAAGGATCACCNT 278  
 Db 280 GGCATTCGCTGACACCATGACCTCTTTGTCGAGCGGTACAGGCAAGGATCACCNT 339

Qy 279 GGAANTAGGAGTAAAGCTAGAGGNTCANTTTCGGAACCACTTANNCTTANAANNAAT 338  
 Db 340 AGTTGCT-GGTGTTGAAGCAGAGGATTCATTTTGGTCTCCCATTCG--ATTAGCCAT 396

Qy 339 TGGTCAAAATGTCGCTGATGAGGCGGNAATNAGTTCGCGGANGCNAATGATTT 395  
 Db 397 AGTGCAAAAGTTGT-TCCAATAAGGAAGCAAAAATAATACCTGGTGGTGATAT 452

RESULT 15  
 BE421015 1206 bp mRNA linear EST 24-JUL-2000  
 LOCUS HW0004.H08 ITEC HWM Barley Leaf Library Hordeum vulgare cDNA clone  
 DEFINITION HW0004.H08, mRNA sequence.  
 ACCESSION BE421015  
 VERSION BE421015.1 GI:9418858  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare.

REFERENCE  
 AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,  
 S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,  
 Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,  
 Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,  
 Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,  
 Sorrells,M., Warburton,M. and Wenzel,G.  
 International Triticeae EST Cooperative (ITEC): Production of  
 Expressed Sequence Tags for Species of the Triticeae  
 Unpublished (2000)

JOURNAL COMMENT  
 Contact: Herrmann RG  
 Botanisches Institut der LMU  
 Menzinger Str. 67, D-80638 Muenchen GERMANY  
 Fax: 49 30 171683  
 Email: hermann@botanik.biologie.uni-muenchen.de  
 International Triticeae EST Cooperative (ITEC)  
 http://wheat.pw.usda.gov/genome.  
 location/Qualifiers

FEATURES  
 source  
 1..1206  
 /organism="Hordeum vulgare"  
 /cultivar="Barke"  
 /db\_xref="taxon:4513"  
 /clone="HW0004.H08"  
 /tissue\_type="leaf"  
 /dev\_stage="14 day old"  
 /note="Vector: pBluescriptSK(-); 850 bp average insert size."

BASE COUNT 294 a 257 c 375 g 280 t  
 ORIGIN

Query Match 28.4%; Score 125; DB 10; Length 1206;  
 Best Local Similarity 64.3%; Pred. NO. 8.4e-23;  
 Matches 207; Conservative 0; Mismatches 108; Indels 7; Gaps 3;

Qy 74 GCGGCGAGGCGGCGGTGGTGGCGATGGCGTNCGCTGATGCGCGCTTGGCGGGA 133  
 Db 43 GAGGCGCGAGGCGTGGCGCGGTTCGCGATGGCATCC---GACGGCGCGTGGAGCGGA 99

Qy 134 TCGNCTCTTCATCCNGGTTNATCCGACTTNCAGGCGAGGATNATGTTTCAGGACA 193  
 Db 100 TCGGCTCCAGCATCCGCGCATCCCACTTCCCAAGCCAGGATTTGTTTCAGGACA 159

Qy 194 TCANGANGTGTGTCGATCCCAAGCGGNTCCGTCAGCAACATATACCATTTTTCAGC 253  
 Db 160 TCACACCTTCTCTCGATCCACGAGCATTCGTCACCCACGACCTTTTGTGGAGC 219

Qy 254 GTTACAGGACCAAGGATCACCNTGGAANTAGGAGTTAAAGCTAGAGGNTCANITTC 313  
 Db 220 GTTACAGGACCAAGGATCACCNTGGAANTAGGAGTTAAAGCTAGAGGNTCANITTC 278

Qy 314 GGAACCACTTANNCTTANAANNAATTTGTCACAAAATNGTNCNATTTAGGAAGCNAAT 373  
 Db 279 GCGCGCGCTATTCGATTTAGCCATAGGTGCGAAGTTTG---TTCCAATTAAGGAAGCGGAA 335

Qy 374 NAGNTGCCANGCNAATGATTT 395  
 Db 336 AAACCTACCTGGTGGAGGTGATAT 357

Search completed: November 30, 2002, 06:27:36  
 Job time : 2093 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 04:02:32 ; Search time 3363 Seconds  
(without alignments)  
3289.532 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 440  
Sequence: 1 cgtccgcgcgcgcgcctc.....ggaaatntagataaaaaant 440

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending Patents NA.Main.\*
- 1: /cgn2\_6/ptodata/1/pna/US06 COMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/pna/US06 COMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pna/US07 COMB.seq.\*
  - 4: /cgn2\_6/ptodata/1/pna/US08 COMB.seq.\*
  - 5: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 6: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 7: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 8: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 9: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 10: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 11: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 12: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 13: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 14: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 15: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 16: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 17: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 18: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 19: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 20: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 21: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 22: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 23: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 24: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 25: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 26: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 27: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 28: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 29: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 30: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 31: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 32: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 33: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 34: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 35: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 36: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 37: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 38: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 39: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 40: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 41: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 42: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*
  - 43: /cgn2\_6/ptodata/1/pna/US09 COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	Description
1	396	90.0	440	16	US-09-227-586-5
2	396	90.0	440	36	US-09-976-054-5
3	275.6	62.6	566	33	US-09-865-439A-110502
4	275.6	62.6	586	33	US-09-865-419A-34849
5	275.6	62.6	586	33	US-09-865-419A-17908
6	275.6	62.6	593	33	US-09-865-419A-40126
7	275.6	62.6	593	64	US-09-865-439A-25058
8	275.6	62.6	626	33	US-09-865-439A-27582
9	267.6	60.8	626	64	US-09-865-439A-10668
10	267.6	60.8	640	27	US-09-207-458-71879
11	267.6	60.8	961	42	US-10-219-999-7177
12	267.6	60.8	961	75	US-10-312-544-3121
13	265.8	60.4	572	33	US-09-513-996A-69703
14	264.4	60.1	572	33	US-09-865-439A-82458
15	264.4	60.1	572	33	US-09-207-458-126600
16	264.4	60.1	961	25	US-09-654-617-266001
17	264.4	60.1	961	27	US-09-684-016-266001
18	262.8	59.7	431	16	US-09-227-586-27
19	262.8	59.7	431	36	US-09-976-054-27
20	262.8	59.7	591	27	US-09-696-664A-11136
21	254.8	57.9	591	27	US-09-696-664A-11136

```
22 254.8 57.9 632 33 US-09-865-439A-79063 Sequence 79063, A
23 254.8 57.9 632 64 US-60-207-458-123205 Sequence 123205, A
24 254 57.0 917 28 US-09-708-427-51979 Sequence 51979, A
25 250.8 57.0 373 17 US-09-304-517A-82318 Sequence 82318, A
26 250.8 57.0 373 17 US-09-371-146A-82318 Sequence 82318, A
27 250.8 57.0 373 17 US-09-985-678-82318 Sequence 82318, A
28 250.8 57.0 375 23 US-09-619-643-11407 Sequence 11407, A
29 250.8 57.0 375 58 US-60-145-485-5266 Sequence 5266, Ap
30 250.8 57.0 410 17 US-09-394-745-7601 Sequence 7601, Ap
31 250.8 57.0 410 22 US-09-565-306-18663 Sequence 18663, A
32 250.2 56.9 560 17 US-09-371-146A-96626 Sequence 96626, A
33 247.2 56.2 479 24 US-09-620-111B-2758 Sequence 2758, Ap
34 244.8 55.6 349 23 US-09-619-643-10988 Sequence 10988, A
35 244.8 55.6 349 58 US-60-145-485-4584 Sequence 4584, Ap
36 244.8 55.6 393 23 US-09-619-643-8571 Sequence 8571, Ap
37 244.8 55.6 393 58 US-60-145-485-1615 Sequence 1615, Ap
38 244.4 55.5 381 17 US-09-304-517A-96626 Sequence 96626, A
39 244.4 55.5 381 17 US-09-394-745-30358 Sequence 30358, A
40 244.4 55.5 381 22 US-09-565-306-49112 Sequence 49112, A
41 244.4 55.5 472 37 US-09-985-678-96626 Sequence 96626, A
42 242.4 55.1 472 16 US-09-227-586-30 Sequence 30, Appl
43 242.4 55.1 472 36 US-09-976-054-30 Sequence 30, Appl
44 239.8 54.5 294 17 US-09-304-517A-33941 Sequence 33941, A
45 239.8 54.5 294 17 US-09-371-146A-33941 Sequence 33941, A

ALIGNMENTS

US-09-227-586-5
; Sequence 5, Application US/09227586A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with the
; FILE REFERENCE: 38-21(15094)B
; CURRENT APPLICATION NUMBER: US/09/227,586A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 711
; SEQ ID NO 5
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
US-09-227-586-5

Query Match 90.0%; Score 396; DB 16; Length 440;
Best Local Similarity 100.0%; Pred. No. 1,2e-99;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C G T C C G C G C G C G C G C A C T T C G C C T T T C G T C C C C G C G C G C G C T C C N N T G A G C 60
DB 1 C G T C C G C G C G C G C G C A C T T C G C C T T T C G T C C C C G C G C G C G C T C C N N T G A G C 60

QY 61 G T G C G C G T C A C C G C G C G C G C G C G C G G T G G T G G C G A T G G C G T N C G C T G A T G C G 120
DB 61 G T G C G C G T C A C C G C G C G C G C G C G C G G C G G T G G T G G C G A T G G C G T N C G C T G A T G C G 120

QY 121 C C G T T G C G G N G A T C G N C T C T N C A T C C N G G T N A T N C C C G A C T T N C C A A G C C A G G G A T N 180
DB 121 C C G T T G C G G N G A T C G N C T C T N C A T C C N G G T N A T N C C C G A C T T N C C A A G C C A G G G A T N 180

QY 181 A T G T T T C A G G A C A T C A N G A N T G T T G C A T C C C A A G G C G N T C C G T G A C A C A T A T A C 240
DB 181 A T G T T T C A G G A C A T C A N G A N T G T T G C A T C C C A A G G C G N T C C G T G A C A C A T A T A C 240

QY 241 C A T T T T G T C A A G C G T T A C A A G C C A A G G N A T C A C C N T G G A A A T A G G A T T A A A G C T A G 300
DB 241 C A T T T T G T C A A G C G T T A C A A G C C A A G G N A T C A C C N T G G A A A T A G G A T T A A A G C T A G 300
```

```
QY 301 A G G G N C A N T T C G G A C A C A C T A N T C T T A N A N N A A T T G G C A A A A A T N G T G C N A T T 360
DB 301 A G G G N C A N T T C G G A C A C A C A C T A N T C T T A N A N N A A T T G G C A A A A A T N G T G C N A T T 360

QY 361 G A G G A G C N N A A T N A G T G C C A N G C N A A A T G A T T T T N A N G A A T A N G A A T T T T N G G A A T N 420
DB 361 G A G G A G C N N A A T N A G T G C C A N G C N A A A T G A T T T T N A N G A A T A N G A A T T T T N G G A A T N 420

QY 421 G G A A T N T A G A T A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A 440
DB 421 G G A A T N T A G A T A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A A 440

RESULT 2
US-09-976-054-5
; Sequence 5, Application US/09976054
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with the
; FILE REFERENCE: 16517,256/38-21(15094)C
; CURRENT APPLICATION NUMBER: US/09/976,054
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: US 60/069,472
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: US 60/071,064
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: US 60/074,201
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 60/074,281
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 60/074,567
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 60/074,565
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 60/075,462
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/075,461
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/075,464
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/075,460
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/075,463
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/077,231
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 60/077,229
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 60/077,230
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 60/078,368
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: US 60/080,844
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/083,067
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: US 60/083,387
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 60/083,388
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 60/085,224
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,223
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,222
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/086,186
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: US 60/086,187
```



;; PRIOR FILING DATE: 1998-05-21  
;; PRIOR APPLICATION NUMBER: US 60/086,185  
;; PRIOR FILING DATE: 1998-05-21  
;; PRIOR APPLICATION NUMBER: US 60/086,184  
;; PRIOR FILING DATE: 1998-05-21  
;; PRIOR APPLICATION NUMBER: US 60/086,188  
;; PRIOR FILING DATE: 1998-05-21  
;; PRIOR APPLICATION NUMBER: US 60/089,524  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: US 60/089,810  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: US 60/089,814  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: US 60/090,170  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: US 60/092,036  
;; PRIOR FILING DATE: 1998-07-08  
;; PRIOR APPLICATION NUMBER: US 60/099,670  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: US 60/099,697  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: US 60/100,674  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: US 60/101,132  
;; PRIOR FILING DATE: 1998-09-21  
;; PRIOR APPLICATION NUMBER: US 60/101,130  
;; PRIOR FILING DATE: 1998-09-21  
;; PRIOR APPLICATION NUMBER: US 60/101,508  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/101,344  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/101,347  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/101,343  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/104,126  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/104,127  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/104,124  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/104,121  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/111,981  
;; PRIOR FILING DATE: 1998-12-11  
;; PRIOR APPLICATION NUMBER: US 09/199,129  
;; PRIOR FILING DATE: 1998-11-24  
;; PRIOR APPLICATION NUMBER: US 09/210,297  
;; PRIOR FILING DATE: 1998-12-08  
;; PRIOR APPLICATION NUMBER: US 09/227,586  
;; PRIOR FILING DATE: 1999-01-08  
;; NUMBER OF SEQ ID NOS: 711  
;; SEQ ID NO 5  
;; LENGTH: 440  
;; TYPE: DNA  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (1)...(440)  
;; OTHER INFORMATION: unsure at all n locations  
US-09-976-054-5

Query Match 90.0%; Score 396; DB 36; Length 440;  
Best Local Similarity 100.0%; Pred. No. 1.2e-99;  
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTCCGCGCGCGGCGACTTCGCTTCCTCCCGCGTCAGCGTCGCGGCTCCNNTGAGC 60  
Db 1 CGTCCGCGCGCGGCGACTTCGCTTCCTCCCGCGTCAGCGTCGCGGCTCCNNTGAGC 60  
Qy 61 GTGCGCGTCACCGCGCGGCGAGGCGGCGGTGTGCGCATGCGCTGCGTGTGATGCG 120  
Db 61 GTGCGCGTCACCGCGCGGCGAGGCGGCGGTGTGCGCATGCGCTGCGTGTGATGCG 120

Qy 121 CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCAAAGCCAGGGATN 180  
Db 121 CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCAAAGCCAGGGATN 180  
Qy 181 ATGTTTCAGGACATCANGANGTNGTTCGATCCCAAGGCGGTCCGTGACAACATATAC 240  
Db 181 ATGTTTCAGGACATCANGANGTNGTTCGATCCCAAGGCGGTCCGTGACAACATATAC 240  
Qy 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATCCACCTTGAAGATAGGAGTTAAAGCTAG 300  
Db 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATCCACCTTGAAGATAGGAGTTAAAGCTAG 300  
Qy 301 AGGGNTCANTTTCGGAACAACCTANNCTTANAANNAATTTGTCAAAAATNGTGNCAATT 360  
Db 301 AGGGNTCANTTTCGGAACAACCTANNCTTANAANNAATTTGTCAAAAATNGTGNCAATT 360  
Qy 361 GAGGACGNNATNAGTCCGANGCNAATGATTTTNANGAATANGAATTTTNGGAATNN 420  
Db 361 GAGGACGNNATNAGTCCGANGCNAATGATTTTNANGAATANGAATTTTNGGAATNN 420  
Qy 421 GGAATNNTAGATAAAAAANT 440  
Db 421 GGAATNNTAGATAAAAAANT 440

## RESULT 3

US-09-865-439A-110502  
; Sequence 110502, Application US/09865439A  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D.  
; APPLICANT: Hardeman, Kristine J.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51936)B  
; CURRENT APPLICATION NUMBER: US/09/865,439A  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/207,458  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 119126  
; SEQ ID NO 110502  
; LENGTH: 566  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(566)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3732-014-Q1-K6-C3  
US-09-865-439A-110502

Query Match 62.6%; Score 275.6; DB 33; Length 566;  
Best Local Similarity 79.1%; Pred. No. 5.1e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;

Qy 1 CGTCCGCGCGCGGCGACTTCGCTTCCTCCCGCGTCAGCGTCGCGGCTCCNNTGAGC 60  
Db 28 CGTCCGCGCGGCGGCGAGCGCGCTTTTCGTCGCCCGCGTCAGCGTCGCGGCTCCACTGAGC 87  
Qy 61 GTGCGCGTCACCGCGCGGCGAGGCGGCGGTGTGCGCATGCGCTGCGTGTGATGCG 120  
Db 88 GTGCGCGTCACCGCGCGGCGAGGCGGCGGTGTGCGCATGCGCTGCGTGTGATGCG 147  
Qy 121 CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCAAAGCCAGGGATN 180  
Db 148 CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCAAAGCCAGGGATN 207  
Qy 181 ATGTTTCAGGACATCANGANGTNGTTCGATCCCAAGGCGGTCCGTGACAACATATAC 240  
Db 208 ATGTTTCAGGACATCAGACGTTGCTGCTGATCCCAAGGCGGTCCGTGACACCATCGAC 267  
Qy 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATCCACCTTGAAGATAGGAGTTAAAGCTAG 300

[illegible]

Query Match	62.6%	Score 275.6	DB 33	Length 586
Best Local Similarity	79.1%	Pred. No. 5.2e-66		
Matches 348	Conservative 0	Mismatches 86	Indels 6	Gaps 4
QY	1	CGTCCGCGCGCGCGAGTTCGTGCTCCCGCGGTACAGCGTCGCGGCTCCNNTGAGC	60	
Db	63	CGTCCGCGCGCGCGAGCGCGCTTTTCGTCCCGCGGTACAGCGTCGCGGCTCCACTGAGC	122	
QY	61	GTGCGGCTCACGGCGGACAGCGAGCGCGTGTGGCGATGGCGTNCGCTCATGTCG	120	
Db	123	GTGCGCTCACCGGCGGACAGCGAGCGCGGTGTGGCGATGGCGTCCGTCATGCG	192	
QY	121	CGCTTGGCGGATGCGNCTCTCNATCCNGGTWATNCCCGACTTNCAGCGCGGATN	180	
Db	193	CGCTTGGCGGATGCGCTCTCCATCCGCGTATCCCGACTTCCCCAAGCGCGGATC	242	
QY	181	ATGTTTCAGGAGCATCANGANGTNGTTCGATCCCAAGCGGNTCCGTGACAACTATAC	240	
Db	243	ATGTTTCAGGAGCATCAGAGGTGTGTCGATCCCAAGGCGTTCGTGACACCATCGAC	302	
QY	241	CATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCTGGAAATAGGAGTTAAAGCTAG	300	
Db	303	CTCTTTGTCAAGCGGTACAGGACCAAGGATCACCGTGGTGTCT-GGTGTTGAAGCTAG	361	
QY	301	AGGNTCANTTTCGACACACTANNTCTTANANNAATTTGGTCAAAAATNGGTGNCNATT	360	
Db	362	AGGTTTCATTTTTTTCGCTCCTCATCGCT--TAGCCATCGGGCAAAATTTGTGCT--TT	418	
QY	361	GAGGAAGCNNATWAGNTGCCANGCNAATCATTTTNNGAATANGAATTTNGGGAATN	420	
Db	419	GAGGAAGCGGAAGAGTTGCCAGGCGAGGTGATCT--CCGAAGAGTATCTTTTGGGAAT	476	

```

QY      421  GGAATNTAGATAAAAAAT 440
      |||||  |  |  |  |  |  |
Db      477  GGAAGTACACAGATAGAAAT 496

RESULT 5
US-60-208-063-17908
; Sequence 17908, Application US/60208063
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lalugudi, Raghunath V.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION:
; FILE REFERENCE: 38-21(51935)A
; CURRENT APPLICATION NUMBER: US/60/208,063
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 25021
; SEQ ID NO 17908
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3600-035-Q6-K6-E7
US-60-208-063-17908

```

Query Match 52.6%; Score 275.6; DB 64; Length 586;  
Best Local Similarity 79.1%; Pred.No. 5.2e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps

	QY	1	GTCTCGGGCGGCGGCAGCTTCGCCCTTTTCTGTCCTCCCGCTCAGCGTCACGGCTCCGCGCTCCNNTCAGC	60
	Dd	63	GTCGCGGGCGGCGGCAGCGCCCTTTTGCTGTCCTCCCGCTCAGCGTCACGGCTCCCACTCAGC	122
	QY	61	GTGGCGCTCACCGCGCGCAGCGCAGGCGGTGGTGGCGATGGCGTNCGCTCATGTGG	120
	Dd	123	GTGGCGCTCACCGCGCGCAGCGCAGGCGGTGGTGGCGATGGCGTNCGCTCATGTGG	182
	QY	121	GCCTTGGCGNGGATCGNCTCTCCATCTCCNCGGTATTNCCCAGCTTNCCAAAGCCAGGGATN	180
	Dd	183	GCCTTGGCGGGGATCGCCTCTCCATCCGCGCTCATCCCGACTTCCCCAAGCCAGGGATC	242
	QY	181	ATGTTTTCAGGACATCANGANGNTGTTTCGATCCGACGGGNTCCGTGCACAATATAC	240
	Dd	243	ATGTTTTCAGGACATCACCAGCTTCTGCTCGATCCCAAGGCGTTCCGTGCACATCGAC	302
	QY	241	CATTTTCTCAAGCGGTACAAGGACCAAGGNATCCNNTGGAAANTAGGAGTTTAAAGTAG	300
	Dd	303	CTCTTTCTCGCGGGTACAAGGACCAAGGGATCAACGGTGGTTGCT--GGTGTGTAAGTAG	361
	QY	301	AGGNTCANNTTTCGGAACCACTANNCTCTTAANNAATTTGGTCAAAAATNGGTGNCNATT	360
	Dd	362	AGGTTTCATTTTCGGTCTCTCATCGCTT--TAGCCATCGCGCAAAATTTCTGCCT-TT	418
	QY	361	GAGGACGNNARTNAGNTGCCANCNCNAATGATTTTNAGAANTANGAATTTTNGGAATNN	420
	Dd	419	GAGGACCGCAGAGAGTTTGGCAGCGGAGGTGATCT--CCGAAGAGTATTCTTTTGGAAAT	476
	QY	421	GGATNNNTAGATAAAAAANT	440
	Dd	477	GSAACTCACAAGATAGAAT	496

```

RESULT 6
US-09-865-419A-40126
; Sequence 40126, Application US/09865419A
; GENERAL INFORMATION:
; APPLICANT: Connet, Timothy W.
; APPLICANT: Wu, Kunsheng

```

```

? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
?
? TITLE OF INVENTION: Plants
?
? FILE REFERENCE: 38-21(51935)B
?
? CURRENT APPLICATION NUMBER: US/09/865,419A
?
? CURRENT FILING DATE: 2001-05-29
?
? PRIOR APPLICATION NUMBER: US 60/208,063
?
? PRIOR FILING DATE: 2000-05-31
?
? NUMBER OF SEQ ID NOS: 54020
?
? SEQ ID NO 40126
?
? LENGTH: 593
?
? TYPE: DNA
?
? ORGANISM: Zea mays
?
? FEATURE:
?
? OTHER INFORMATION: Clone ID: LIB3601-011-PI-K6-A5
?
? US-09-865-419A-40126

```

Query Match 62.6%; Score 275.6; DB 33; Length 593;  
Best Local Similarity 79.1%; Pred. No. 5.2e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;

QY	1	GTCTCGCGCGCGCGACGATTCGCGCTTTCTGTCGCCGCGTCAGCGCTCGCGGCTCCNNNTGAGC	60
Db	34	GTCTCGCGCGCGCGCGACGCGCCCTTTTCGTCCCGCGTCAGCGCTCGCGGCTCCACTGAGC	93
QY	61	GTGCGCGCTACCGCGCGCAGCGCAGGCGGTGGTGGCGATGCGCTNCGCGTGAATGCG	120
Db	94	GTGCGCGCTACCGCGCGCAGCGCAGGCGGTGGTGGCGATGCGCTCGCTGAATGCG	153
QY	121	CGCTTGGCGGNGATCGNCTCTCTNCATCCNGGTNATNCCGACNTTCCAAAGCCAGGGATN	180
Db	154	CGCTTGGCGGNGATCGCTCTCTATCCGCGTCATCCCGCGACTTCCCAAGCAGGAGATC	213
QY	181	ATGTTTCAGACATCATGANGANTGNTGTTGATCCCAAGCGNCTCGTGCAACATATAC	240
Db	214	ATGTTTTCAGGACATCACAGCGTTGCTGCTCGATCCCAAGCGTTCGCTGACACCATCGAC	273
QY	241	CATTTTGTCAAGCGGTACAAGGACCAAGGATNATCACCTTGGAAANTAGGAGTTTAAAGCTAG	300
Db	274	CTCTTTGTCCAGCGGTACAAGGACCAAGGATCATCCGTGGTTGCT - GGTGTGTGAAGCTAG	332
QY	301	AGGNTCANTTTTCGGAACAACATANNCTTTANANNNAATTCGTCARAANTNGTGNCNATT	360
Db	333	AGGCTTCATTTTCGCTCCTATCGCTT - TAGCCATCGGCCCAAAATTTGTGCCT - TT	389
QY	361	GAGGAACNNNAATNAGNTGCCANGCNAATGATTTTNGAARTANGAATTTTNGGAATNN	420
Db	390	GAGGAGCGCGAAGAGTTGGCAGCGAGGTGATCT - CCGAAGAGATTTCTTTTGGAAATAT	447
QY	421	GGAAATNNTAGATAAAAAAANT	440
Db	448	GGAACTGACAAGATAGAAAT	467

```

RESULT 7
US-60-208-063-23182
: Sequence 23182, Application US/60208063
: GENERAL INFORMATION:
: APPLICANT: Andersen, Scott E.
: APPLICANT: Connors, Timothy W.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Laloudi, Raghnath V.
: APPLICANT: Ruff, Thomas G.
: APPLICANT: Shukla, Hridayabhiraunjan
: APPLICANT: Wu, Kunsheng
: APPLICANT: Xu, Nanfei
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
: TITLE OF INVENTION: PLANTS
: FILE REFERENCE: 38-21(51935)A
: CURRENT APPLICATION NUMBER: US/60/208,063
: CURRENT FILING DATE: 2000-05-31
: NUMBER OF SEQ ID NOS: 25021
: SEQ ID NO 23182
: LENGTH: 593

```

```

; TYPE: DNA
; ORGANISM: zea mays
; OTHER INFORMATION: Clone ID: LIR3601-011-P1-K6-A5
US-60-208-063-23182

```

Query Match 62.6%; Score 275.6; DB 64; Length 593;  
Best Local Similarity 79.1%; Pred. No. 5.2e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;

Qy	1	CGTCGCGCGCGCGGACATTCGCGCTTTTGTGTCGCCCGCGTCAAGCGTCGCGGCTCCNNTGAGC	60
Db	34	CGTCGCGCGCGCGCGGACGCGGCTTTTGTGTCGCCCGCGTCAAGCGTCGCGGCTCCATGAGC	93
Qy	61	GTGCGCGTCACCGCGCGGAGCGGCGAGCGGTGTGTGGCGATGCGTTCGCGTCAATGCG	120
Db	94	GTGCGCGTCACCGCGCGGAGCGGCGAGCGGTGTGTGGCGATGCGTTCGCGTCAATGCG	153
Qy	121	CGCTTGCGCGGATCGCTTCCTCATCCNGGTNATCCGACATTNCCAAAGCCAGGGATN	180
Db	154	CGCTTGCGGGGATCGCTTCCTCATCCCGGTCATCCCGGACTTCCCAAGCCAGGGATC	213
Qy	181	ATGTTTCAGGACATCANGANGNTGTTTCGATCCCAAGCGNATCCGTGACACATATAC	240
Db	214	ATGTTTCAGGACATCAGCACGTTTCTGCTCGATCCCAAGCGTTCGGTGACACCATCGAC	273
Qy	241	CATTTTCTCAAGCGGTACAAGGACCAAGGNATCAACNTGGAAANTAGGAGTTTAAAGTAG	300
Db	274	CTCTTTCTCGAGCGGTACAAGGACCAAGGATACCGGTGTTGCT--GGTGTGTAGCTAG	332
Qy	301	AGGGTCANTTTTCGGAACCACTANNCTTTANAANNAATGGTCAAAATNGTGNCNATT	360
Db	333	AGGGTTCATTTCGGTTCCTCTATCGCTT--TAGCCATCGGCGCAAAATTTGTGCCT--TT	399
Qy	361	GAGGAACGNNATNAGNTGCCANGCNAATGATTTTNTANGAATANGAAATTTTNGGAATN	420
Db	390	GAGGAGCGCAGAGAGTTTGCCAGCGGAGGTGATCT--CCGAAGAGTATTTCTTTTGGAAAT	447
Qy	421	GGAATNNTAGATAAAAAANT	440
Db	448	GGAACTCACAAGATAGAAAT	467

```

RESULT 8
US-10-219-999-25058
? Sequence 25058, Application US/10219999
? GENERAL INFORMATION:
? APPLICANT: Cao, Yongwei
? APPLICANT: Edgerton, Michael D
? APPLICANT: Hinkle, Gregory J.
? APPLICANT: Kovalic, David K.
? APPLICANT: Liu, Jingdong
? APPLICANT: Stein, Joshua
? TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
? FILE REFERENCE: 38-10/52726VC
? CURRENT APPLICATION NUMBER: US/10/219, 999
? CURRENT FILING DATE: 2002-08-15
? PRIOR APPLICATION NUMBER: US 60/324, 109
? PRIOR FILING DATE: 2001-09-21
? PRIOR APPLICATION NUMBER: US 60/312,544
? PRIOR FILING DATE: 2001-08-15
? NUMBER OF SEQ ID NOS: 63520
? SEQ ID NO 25058
? LENGTH: 892
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (2)..(697)
? OTHER INFORMATION:
US-10-219-999-25058

```

Query Match 62.6%; Score 275.6; DB 42; Length 892;  
Best Local Similarity 79.1%; Pred. No. 6.1e-66;

QY	181	ATGTTTCAGGACATCANGANGNTGNTGTCGATCCCAAGCGGNTCCGTTGACACAFATAC	241
DB	186	ATGTTTCAGGACATCANGAGTGTGCTGCTGATCCCAAGCGGTTCCGTTGACACCAATCGAC	245
QY	241	CATTTTGTCAAGCGGTACAAGGACCAGGNNATCACCVNTGGAANTAGGAGTTAAAGCTAG	300
DB	246	CTCTTTGTTCGAGCGGTACAAGGACCAGGAGATCACCGTGGTGTCT--GTGTGTTGAAGCTAG	304
QY	301	AGGNTCANTTTTCGGAACAACACTANNCTTTTANAANAATTTGGTCAAAAAATNGTGCNCAAT	360
DB	305	AGGGTTTCANTTTTGTGCTCTCTCTATCGCTT--TAGGCCATTGGCGCAAAATTTGTGCCT--TT	361
QY	361	GAGGAAGCNAATNANGNTGGCANGCNAATGATTTTNAAGAATFANGAATTTTNGGAATNN	420
DB	362	GAGGAAGCCCAAGAAAGTTGCCAGCGAGGTGATCT--CCGAAGAGTATTCTTTTGGAAAT	419
QY	421	GGAATNTAGATAAAAAAT 440	
DB	420	GGAACGACAGATAGAAAT 439	

```

RESULT 10
US-60-207-458-71879
: Sequence 71879, Application US/60207458
: GENERAL INFORMATION:
: APPLICANT: Abad, Mark S.
: APPLICANT: Conner, Timothy W.
: APPLICANT: Deikman, Jill
: APPLICANT: Hardeman, Kristine J.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Lalquidi, Radhunath V.
: APPLICANT: Ruan, Yijun G.
: APPLICANT: Ruff, Thomas G.
: APPLICANT: Sammons, R. Douglas
: APPLICANT: Shukla, Hridayabhiranjan
: APPLICANT: Wu, Kunsheng
: APPLICANT: Xu, Nanfei
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES AS
: FILE REFERENCE: 38-21(51936)A
: CURRENT APPLICATION NUMBER: US/60/207,458
: CURRENT FILING DATE: 2000-05-30
: NUMBER OF SEQ. ID NOS: 152403
: SEQ. ID NO 71879
: LENGTH: 626
: TYPE: DNA
: ORGANISM: Zea mays
: OTHER INFORMATION: Clone ID: LTB3354-015-PI-KI-A8
US-60-207-458-71879

Query Match 60.8%; Score 267.6; DB 64; Length 626;
Best Local Similarity 78.0%; Pred. No. 9.1e-64;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps

QY 1 CGTCCGCGCCGCGCGAGCTTCGCTTTTGTCCCGCGCTCAGGCTCGCGCTCCGCTCCACTGAGC 65
DB 6 CGTCCGCGCCGCGCGAGCGCTTTTGTCTCCCGCGCTCAGCGTTCGCGCTCCACTGAGC 65
QY 61 GTGCGCGTCACGCGCGCAGGCGAGCGGTGTGTCGATGGCTTCGCTGATGCG 120
DB 66 GTGCGTGTACCGCGCGGAGGCGAAGGCGAGCGGTGTGGCGATGGCTCCGCTGACGCG 125
QY 121 CGCTGGCGGAGATCGNCTCTCNATCCNGTNTATNCCGACTTTCACAAACCCAGGGATN 180
DB 126 CGCTTGGCGGGGATCGGCTCTCTCATCCGCGGTATCCCGGACTTCCCAAGCCAGGGATC 185
QY 181 ATGTTTCAGGACATCANGANGNTGNTGTTGATCCCAAGCGGNTCCGTTGACACAFATAC 240
DB 186 ATGTTTCAGGACATCAGGAGTGTGCTGCTGATCCCAAGCGGTTCCGTTGACACCAATCGAC 245
QY 241 CATTTTGTCAAGCGGTACAAGGACCAGGNNATCACCVNTGGAANTAGGAGTTAAAGCTAG 300

```

```
Db 246 CTCTTTGTCGAGCGGTACAAGGACCAAGGGATCACCGGTGGCT-GGTGTGAAGCTAG 304
Qy 301 AGGNTCANTTTCCGAACAACACTANNCTTANAANNAATTTGGTCAAAAATNGTGCNATT 360
Db 305 AGGGTTCAATTTTGGTCTCTCTATCGCTT--TAGCCATTGGCGCAAAATTTGTGCCT-TT 361
Qy 361 GAGGAAGCNAATNAGTGGCCAGGAAATCATTTTANCAATANGAATTTTNGGAATNN 420
Db 362 GAGGAAGCGGAGAGTGGCCAGCGAGGTGATCT--CCGAGAGATATTCTTTGGAAATAT 419
Qy 421 GGAATNTAGTAAAAAANT 440
Db 420 GGAAGTGAAGATAGAAAT 439

RESULT 11
US-09-696-664A-10668
; Sequence 10668, Application US/09696664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 10668
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(640)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB379-182-Q1-R6-A2
US-09-696-664A-10668

Query Match 60.8%; Score 267.6; DB 27; Length 640;
Best Local Similarity 78.0%; Pred. No. 9.1e-64;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy 1 CGTCCGCGCGCGGCTTCGCTTTTCGTCGCGCGGTCCAGCGTCGCGGCTCCNNTGAGC 60
Db 6 CGTCCGCGCGCGGCGAGCGCGCTTTTCGTCGCGCGGTCCAGCGTCGCGGCTCCACTGAGC 65
Qy 61 GTGCGGCTCACCGCGCGGAGGAGGCGGTGGTGGCGATGGCGTNCGTGATCG 120
Db 66 GTGCGGCTCACCGCGCGGAGGAGGAGGCGGTGGTGGCGATGGCGTNCGTGATCG 125
Qy 121 CGCTTGGCGGNGATCGNCTCCTTCATCCNGGTNATNCCCGACTTNCACCAAGCCAGGGATN 180
Db 126 CGCTTGGCGGNGATCGNCTCCTTCATCCNGGTNATNCCCGACTTNCACCAAGCCAGGGATN 185
Qy 181 ATGTTTTCAGGACATCANGANGTGTGTCGATCCCAAGCGGTTCGTCGATCCCAAGCCAGGGATN 240
Db 186 ATGTTTTCAGGACATCANGANGTGTGTCGATCCCAAGCGGTTCGTCGATCCCAAGCCAGGGATN 245
Qy 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATCACCNTGGAANTAGAGTTAAAGCTAG 300
Db 246 CTCCTTTGTCAAGCGGTACAAGGACCAAGGATCACCNTGGAANTAGAGTTAAAGCTAG 304
Qy 301 AGGNTCANTTTCCGACAACTANNCTTANAANNAATTTGGTCAAAAATNGTGCNATT 360
Db 305 AGGGTTCAATTTTGGTCTCTCTATCGCTT--TAGCCATTGGCGCAAAATTTGTGCCT-TT 361
Qy 361 GAGGAAGCNAATNAGTGGCCAGGAAATCATTTTANCAATANGAATTTTNGGAATNN 420
Db 362 GAGGAAGCGGAGAGTGGCCAGCGAGGTGATCT--CCGAGAGATATTCTTTGGAAATAT 419
```

```
Db 362 GAGGAAGCGGAGAGTGGCCAGCGAGGTGATCT--CCGAGAGATATTCTTTGGAAATAT 419
Qy 421 GGAATNTAGTAAAAAANT 440
Db 420 GGAAGTGAAGATAGAAAT 439

RESULT 12
US-10-219-999-7177
; Sequence 7177, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Jishua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)C
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 7177
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(656)
; OTHER INFORMATION:
US-10-219-999-7177

Query Match 60.8%; Score 267.6; DB 42; Length 961;
Best Local Similarity 78.0%; Pred. No. 1.1e-63;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy 1 CGTCCGCGCGCGGCTTCGCTTTTCGTCGCGCGGTCCAGCGTCGCGGCTCCNNTGAGC 60
Db 12 CGTCCGCGCGCGGCGAGCGCGCTTTTCGTCGCGCGGTCCAGCGTCGCGGCTCCACTGAGC 71
Qy 61 GTGCGGCTCACCGCGCGGAGGAGGCGGTGGTGGCGATGGCGTNCGTGATCG 120
Db 72 GTGCGGCTCACCGCGCGGAGGAGGAGGCGGTGGTGGCGATGGCGTNCGTGATCG 131
Qy 121 CGCTTGGCGGNGATCGNCTCCTTCATCCNGGTNATNCCCGACTTNCACCAAGCCAGGGATN 180
Db 132 CGCTTGGCGGNGATCGNCTCCTTCATCCNGGTNATNCCCGACTTNCACCAAGCCAGGGATN 191
Qy 181 ATGTTTTCAGGACATCANGANGTGTGTCGATCCCAAGCGGTTCGTCGATCCCAAGCCAGGGATN 240
Db 192 ATGTTTTCAGGACATCANGANGTGTGTCGATCCCAAGCGGTTCGTCGATCCCAAGCCAGGGATN 251
Qy 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATCACCNTGGAANTAGAGTTAAAGCTAG 300
Db 252 CTCCTTTGTCAAGCGGTACAAGGACCAAGGATCACCNTGGAANTAGAGTTAAAGCTAG 310
Qy 301 AGGNTCANTTTCCGACAACTANNCTTANAANNAATTTGGTCAAAAATNGTGCNATT 360
Db 311 AGGGTTCAATTTTGGTCTCTCTATCGCTT--TAGCCATTGGCGCAAAATTTGTGCCT-TT 367
Qy 361 GAGGAAGCNAATNAGTGGCCAGGAAATCATTTTANCAATANGAATTTTNGGAATNN 420
Db 368 GAGGAAGCGGAGAGTGGCCAGCGAGGTGATCT--CCGAGAGATATTCTTTGGAAATAT 425
Qy 421 GGAATNTAGTAAAAAANT 440
Db 426 GGAAGTGAAGATAGAAAT 445
```

Mon Dec 2 12:27:39 2002

```
RESULT 13
US-60-312-544-3121
; Sequence 3121, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 3121
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(656)
; OTHER INFORMATION: Clone ID: LIB3068-059-H7_FLI
US-60-312-544-3121

Query Match 60.8%; Score 267.6; DB 75; Length 961;
Best Local Similarity 78.0%; Pred. No. 1.le-63;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

QY 1 CGTCCGCGCGCGGACTTCGCTTTTCGTCGCCGCTCAGCGTCGCGGCTCCNNTCAGC 60
DB 12 CGTCCGCGCGCGGCGCGGCTTTTCGTCGCCGCTCAGCGTCGCGGCTCCACTGAGC 71
QY 61 GTGGCGGTCAACGGCGGAGGCGAGGCGGTGGTGGCGATGCGTGGCTGATGCG 120
DB 72 GTGGCGGTCAACGGCGGAGGCGAGGCGGTGGTGGCGATGCGTGGCTGATGCG 131
QY 121 CGCTTGGCGGATCGNCTCTNCATCGCTGATGCGTGGTGGCGATGCGTGGCTGATGCG 180
DB 132 CGCTTGGCGGATCGNCTCTNCATCGCTGATGCGTGGTGGCGATGCGTGGCTGATGCG 191
QY 181 ATGTTTCAGGACATCANGANGTGTTCGATCCCAAGGCGTTCGCGTACACATATAC 240
DB 192 ATGTTTCAGGACATCANGANGTGTTCGATCCCAAGGCGTTCGCGTACACATATAC 251
QY 241 CATTTTGTCAAGCGGTACAGGACCAAGGATGCGTGGTGGCGATGCGTGGCTGATGCG 300
DB 252 CATTTTGTCAAGCGGTACAGGACCAAGGATGCGTGGTGGCGATGCGTGGCTGATGCG 310
QY 301 AGGCGTCAATTTTCGCAACACTANNTCTTANANNAATGTCACAAATNGTGNCNATT 360
DB 311 AGGCGTCAATTTTCGCAACACTANNTCTTANANNAATGTCACAAATNGTGNCNATT 367
QY 361 GAGGAACNNATNAGTCCGANGCNAATGATTTTNGANGAATNANGAATTTTNGAATNN 420
DB 368 GAGGAACNNATNAGTCCGANGCNAATGATTTTNGANGAATNANGAATTTTNGAATNN 425
QY 421 GGAATNNTAGATAAAAAANT 440
DB 426 GGAATNNTAGATAAAAAANT 445

RESULT 14
US-09-513-996A-69703
; Sequence 69703, Application US/09513996A
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-709P
; CURRENT APPLICATION NUMBER: US/09/513,996A
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 81028
```

```
; SEQ ID NO 69703
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 1..462
; OTHER INFORMATION: any n or Xaa = unknown
; FEATURE:
; OTHER INFORMATION: Location 1..462 / Ceres Seq. ID 2191602
US-09-513-996A-69703

Query Match 60.4%; Score 265.8; DB 19; Length 462;
Best Local Similarity 79.5%; Pred. No. 2.5e-63;
Matches 337; Conservative 0; Mismatches 81; Indels 6; Gaps 4;

QY 1 CTTCCGCGCGCGGCGACTTCGCTTTTCGTCGCCGCTCAGCGTCGCGGCTCCNNTCAGC 60
DB 42 CTTCCGCGCGCGGCGACTTCGCTTTTCGTCGCCGCTCAGCGTCGCGGCTCCACTGAGC 101
QY 61 GTGGCGGTCAACGGCGGAGGCGAGGCGGTGGTGGCGATGCGTGGCTGATGCG 120
DB 102 GTGGCGGTCAACGGCGGAGGCGAGGCGGTGGTGGCGATGCGTGGCTGATGCG 161
QY 121 CGCTTGGCGGATCGNCTCTNCATCGCTGATGCGTGGTGGCGATGCGTGGCTGATGCG 180
DB 162 CGCTTGGCGGATCGNCTCTNCATCGCTGATGCGTGGTGGCGATGCGTGGCTGATGCG 221
QY 181 ATGTTTCAGGACATCANGANGTGTTCGATCCCAAGGCGTTCGCGTACACATATAC 240
DB 222 ATGTTTCAGGACATCANGANGTGTTCGATCCCAAGGCGTTCGCGTACACATATAC 281
QY 241 CATTTTGTCAAGCGGTACAGGACCAAGGATGCGTGGTGGCGATGCGTGGCTGATGCG 300
DB 282 CATTTTGTCAAGCGGTACAGGACCAAGGATGCGTGGTGGCGATGCGTGGCTGATGCG 340
QY 301 AGGCGTCAATTTTCGCAACACTANNTCTTANANNAATGTCACAAATNGTGNCNATT 360
DB 341 AGGCGTCAATTTTCGCAACACTANNTCTTANANNAATGTCACAAATNGTGNCNATT 397
QY 361 GAGGAACNNATNAGTCCGANGCNAATGATTTTNGANGAATNANGAATTTTNGAATNN 420
DB 398 GAGGAACNNATNAGTCCGANGCNAATGATTTTNGANGAATNANGAATTTTNGAATNN 455
QY 421 GGA 424
DB 456 GGA 459

RESULT 15
US-09-865-439A-82458
; Sequence 82458, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 82458
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3606-028-Q1-K6-C4
US-09-865-439A-82458

Query Match 60.1%; Score 264.4; DB 33; Length 572;
```







GenCore version 5.1.3

Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 02:40:12 : Search time 267 seconds  
(without alignments)

3711.158 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtccgcgcgcgcgcgccttc.....ggaatnntagataaaaaaant 440

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_101002:\*

- 1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*
- 2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*
- 17: /SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*
- 18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	265.8	50.4	462	21 AAC51765	Zea mays DNA fragm
2	225	51.1	455	21 AAC51740	Zea mays DNA fragm
3	95.6	22.6	405	21 AAC43563	Zea mays DNA fragm
4	90.4	20.5	380	21 AAA31767	Plant microsattelli
5	88.4	20.1	1034	21 AAC49172	Arabidopsis thalia
6	88.4	20.1	1036	21 AAC35980	Arabidopsis thalia
7	88.2	20.0	729	14 AAC35208	Sequence encoding
8	86.8	19.7	1036	21 AAC40946	Arabidopsis thalia
9	86.6	19.7	821	21 AAC33967	Arabidopsis thalia

10	85	19.3	780	21	AAC40942	Arabidopsis thalia
11	85	19.3	821	21	AAC40945	Arabidopsis thalia
12	77	17.5	552	21	AAC43276	Arabidopsis thalia
13	77	17.5	847	21	AAC45129	Arabidopsis thalia
14	72.4	16.5	459	21	AAC46344	Arabidopsis thalia
15	72.4	16.5	549	21	AAC42993	Arabidopsis thalia
16	69	15.7	579	21	AAC44711	Arabidopsis thalia
17	67.8	15.4	372	21	AAC46302	Arabidopsis thalia
18	67.8	15.4	1337	21	AAC45318	Arabidopsis thalia
19	67.8	15.4	1348	21	AAC34911	Arabidopsis thalia
20	63.8	14.5	945	24	ABN98579	Arabidopsis thalia
21	43.6	9.9	376	22	AAK59140	Human immune/hagma
22	40.2	9.1	18477	23	AAK59634	Propionibacterium
23	39	8.9	109519	22	AA308693	Micromonospora DNA
24	38.2	8.7	390	24	ABN21436	Human OREF polynuc
25	38.2	8.7	2803	22	AAH54984	S. epidermidis gen
26	38.2	8.7	3002	22	AAH54052	S. epidermidis gen
27	38	8.6	7178	21	AAV59145	DNA encoding a pep
28	37.4	8.5	17555	19	AAV56642	Actinoplanes sp. a
29	37.2	8.5	6072	24	ABL32030	Human immune syate
30	36.8	8.4	423	23	AA572516	DNA encoding novel
31	36.8	8.4	423	23	AA591898	DNA encoding novel
32	36.8	8.4	4403765	22	AAI99683	Mycobacterium tube
33	36	8.2	469	21	AAC38332	Zea mays DNA fragm
34	36	8.2	2464	23	AA586119	DNA encoding novel
35	35.2	8.0	4411529	22	AAI99682	Mycobacterium tube
36	35	8.0	888	22	AAH51974	Mycobacterium tube
37	35	8.0	888	24	ABK14303	DNA encoding proli
38	35	8.0	2209	24	ABK14301	DNA encoding proli
39	35	8.0	5181	24	ABL68935	Kidney cancer rela
40	35	8.0	4403765	22	AAI99683	Mycobacterium tube
41	35	8.0	4411529	22	AAI99682	Mycobacterium tube
42	34.8	7.9	3076	19	AAV43674	Receptor type tyro
43	34.8	7.9	3441	18	AAH87922	Rat cerebellum der
44	34.8	7.9	65140	22	AAD17184	Streptomyces nous
45	34.8	7.9	125401	22	AAD17186	Streptomyces nous

## ALIGNMENTS

RESULT 1  
AAC51765  
ID AAC51765 standard; DNA; 462 BP.  
AC AAC51765;  
AC AAC51765;  
DT 18-OCT-2000 (first entry)  
XX  
XX  
XX Zea mays DNA fragment SEQ ID NO: 69703.  
DE  
DE  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.  
XX  
XX Zea mays subsp. mays.  
XX  
XX  
PN EP1033405-A2.  
XX  
XX  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 10-JUN-1999; 99US-0139919.  
PR 14-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142300.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.

PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145114.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147304.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 16-AUG-1999; 99US-0149175.  
PR 17-AUG-1999; 99US-0148426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.

PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 60.4%; Score 265.8; DB 21; Length 462;

Best Local Similarity 79.5%; Pred. No. 8e-67;

Matches 337; Conservative 0; Mismatches 81; Indels 6; Gaps 4;

QY 1 C G T C C G C G C G C G C A C T T G C C C T T T T T G C C C G C G T C A G C G T C G C G C T C C N N T G A G C 60  
 D b 42 C G T C C G C G C G C G C A C C G C G C T T T T G C C C G C G T C A G C G T C C G C G C T C C A C T G A G C 101  
 QY 61 C T G C G C G T C A C C G C G C G C A G G C G G T G G T G C G G A T G C G T C G C T G A T G C G 120  
 D b 102 G T G C G T C A C C G C G C G G A G G C A G G C G G T G G T G G C G A T G C G T C C G C T G A C C G C G 161  
 QY 121 C G C T T G C G G N A T C G N C T C T C N C A T C C N G N A T N C C G A C T T C C A A G C C A G G G A T N 180  
 D b 162 C G C T T G C G G G A T C G C T C C T C C A T C C G C G C A T C C C C C A G C T T C C C C A G C C A G G A T C 221  
 QY 181 A T G T T C A G C A T C A N G A N T G T T C G A T C C A A G C G N T C G T G A C A C A T A T A C 240  
 D b 222 A T G T T C A G C A T C A C G A C G T T G T C T C G A T C C A A G C G T T C C G T G A C C A C A T C G A C 281  
 QY 241 C A T T T T C A A G C G T A C A A G C A C A A G N A T C A C C N T G G A A A N T A G G A T T A A A G C T A G 300  
 D b 282 C T C T T T C A G C G T A C A A G C A C A A G G A T C A C C G T G T G C T - G G T G T T G A A G C T A G 340  
 QY 301 A G G N T C A T T T C G A A C A C T A N T C T T A N A A N A A T T G S T C A A A A T N G T C N A T T 360  
 D b 341 A G G C T C A T T T T G T C C T C T A T C G C T T - T A G C A T T G C G C A A A T T G T C C T - T T 397  
 QY 361 G A G A C C N A T N A G N C C A N G A A T G A T T T N A N G A A T A N G A A T T T N G A T N N 420  
 D b 398 G A G A C C C A A G A A G T T G C C A G C G A G G T G A T C T - C C G A G A G T T C T T T G G A A T A T 455  
 QY 421 G G A A 424  
 D b 456 G G A A 459

RESULT 2

AAC51740

ID AAC51740 standard; DNA; 455 BP.

AC AAC51740;

XX AAC51740;

DT 18-OCT-2000 (first entry)

DE Zea mays DNA fragment SEQ ID NO: 69614.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic;  
 pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126284.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 23-APR-1999; 99US-0130891.

XX 28-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 30-APR-1999; 99US-0132407.

XX 04-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 06-MAY-1999; 99US-0132487.

XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 16-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139492.

XX 18-JUN-1999; 99US-0139494.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139750.

XX 21-JUN-1999; 99US-0139817.

XX 22-JUN-1999; 99US-0139899.

XX 23-JUN-1999; 99US-0140353.

XX 23-JUN-1999; 99US-0140354.

[illegible]

```
QY 380 CCAGCNAATGATT 395
    ||| ||| ||| |||
Db 440 CCAGCGAGGTGATCT 455

RESULT 3
AAC43563
ID AAC43563 standard; DNA; 405 BP.
XX
AC AAC43563;
XX
DT 17-OCT-2000 (first entry)
XX
ZE Zea mays DNA fragment SEQ ID NO: 39686.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 15-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 04-MAY-1999; 99US-0132048.
PR 05-MAY-1999; 99US-0132407.
PR 06-MAY-1999; 99US-0132484.
PR 07-MAY-1999; 99US-0132485.
PR 08-MAY-1999; 99US-0132486.
PR 09-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
```

```
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 22.68; Score 99.6; DB 21; Length 405;
Best Local Similarity 83.8; Pred. No. 7.5e-19;
Matches 114; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 1 CGTCCGCGCGCGGACTTCGCTTTTCGTCGCCCGCGTCACGCTCGCGCTCCNNTGAGC 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 25 GGTCCGCKCGCGCGACGCCCTTTTCGTCGCCCGCGTCASS--YCGCGCTCCACTGAGC 82
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GTGCGCTGACCGCGCGGAGGCGGTGGTGGGATGGCGTNCGCTGATCG 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
DB 83 GTGCGTGTACCGCGCGGAGCAAGGCGCGGTGGTGGCGATGGCTCCGCTGACSSG 142
QY 121 CGCTTGGCGGNGATCG 136
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 143 CGCTTGGCGGGAATTG 158

RESULT 4
AAA31767
ID AAA31767 standard; DNA; 380 BP.
XX
AC AAA31767;
XX
DT 05-JUL-2000 (first entry)
XX
DE Plant microsatellite marker #728.
XX
KW Plant microsatellite sequence; core repeat sequence; detection; probe;
KW DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KW variety identification; genetic variability evaluation; primer; ss.
XX
OS Eucalyptus grandis.
XX
PN W09967421-Al.
XX
PD 29-DEC-1999.
XX
PF 25-JUN-1999; 99WO-NZ00092.
XX
PR 25-JUN-1998; 98US-0105307.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Havukkala IJ, Bloksberg LN, Glenn M;
XX
DR WPI; 2000-116958/10.
XX
PT New plant microsatellite markers and associated flanking species for
PT the detection of polymorphic genetic markers -
XX
PS Claim 1; Page 291; 392pp; English.
XX
CC Sequences AAA31040-A32093 represent novel plant microsatellite sequences
CC and associated flanking species. The sequences comprise a central core
CC repeat sequence, especially selected from the sequences AAA32094-A32096
CC with left and right flanking sequences. The polynucleotide sequences
CC can be used in the detection of DNA polymorphisms, in genome mapping,
CC in physical mapping, in positional cloning of genes, in variety
CC identification and in evaluation of genetic variability within and
CC between plant tissues, populations, cultivars, species and species
CC groups. They may also be used to design hybridization probes for
CC oligonucleotide fingerprinting and library screening and to design
CC primers for microsatellite-primed PCR. Microsatellite markers are
CC useful to locate specific economically useful genes in plant genomes.
XX
SQ Sequence 380 BP; 76 A; 103 C; 88 G; 113 T; 0 other;

Query Match 20.5%; Score 90.4; DB 21; Length 380;
Best Local Similarity 57.0%; Pred. No. 3.3e-16;
Matches 142; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 81 GCGAGGCGCGGTGGTGGCGATGGCGTNGCGTGGCGGNGATCGNCTC 140
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 110 GCAGATACACATGCGTCCCAAGCGGTACAGCCCTCGTCTCGCAAGATCGCTC 169
QY 141 CTNCTCCNGTNNATNCCGACTTNCCTCAAGCGAGGATNATGTTTCAGGACATCANGAN 200
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 170 TTGATCCCGCTACATCCGAGATTCCCAAGCCAGGAGTTATGTTTCAGGATATAAGGAC 229
QY 201 GNTGNTGTTTCGATCCCAAGCGGNTCCGTGACACATATACCATTTGTCAAGCGGTACAA 260
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 230 GTTGCTTCTTAATCCTCAGGCGTTTAAGGATACTATTGATCTCTTTGTCGAGAGGTACAG 289
```

[illegible]





PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137502.  
PR 04-JUN-1999; 99US-0137728.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 14-JUN-1999; 99US-0138847.  
PR 16-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 17-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139494.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0145386.  
PR 02-AUG-1999; 99US-0145388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151086.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159325.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 21-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.

```
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 20.1%; Score 88.4; DB 21; Length 1036;
Best Local Similarity 53.7%; Pred. No. 2e-15;
Matches 198; Conservative 0; Mismatches 167; Indels 4; Gaps 3;

QY 69 CACCGCGCGCAGGCGGAGGCGGTGGTGGCGATGCGTNCGTGCGCGCTGGC 128
DB 277 CCGCCGACGATCGGGACACTGAATGCGGACTGAAGATGCAAGATCCCAAGATCGC 336
QY 129 GGNATCGNCTCTNCATCCNGTNCATCCGACTTCCAGCCAGGATNATGTTTCA 188
DB 337 TAAGATTGGCTCTTCCATTAGAGTCATCCCGGACTTCCCTTAACAGGAATCATGTTTCA 396
QY 189 GGACATCANGANGTNGTGTTCGATCCCAAGCGNCTCCGTCACACATATACCATTTGT 248
DB 397 GGACATAACGAGCTTCTCTCGACACTGAGGCCCTTTAAGGATACTATTGCTTTGTTGT 456
QY 249 CAAGCGGTACAAGGACCAAGGNATCACCNNTGAAATAGGAGTTTAAAGCTAGAGGNTCA 308
DB 457 TGATAGATACAAAGATAAAGGCATATCTGTTG--TTGCAGGTGTTGAAGCTAGAGTTTCA 515
QY 309 NTTCGCAACACTANNCTTANAANNAATTTGTCAAAAATNGTGNCAATGAGGAAGC 368
DB 516 TTTTGGCCCTCTATTCGTTG--GCTATTGTTGCCAAATTTGTTCCCA--TGAGGAAGC 572
QY 369 NNAATNGTGCAGCNAATGATTTTNGAANTANGAATTTTNGAATNNGGAATNNT 428
DB 573 CCAAGAAGCTACCTGGGAAGGTATTTCGGAGGAGTATTCCTGGAGGAGTATTCCTGGAGATGGAACAGATA 632
QY 429 AGATAAAAA 437
DB 633 CGATTGAGA 641

RESULT 7
AAC35208
ID AAC35208 standard; cDNA; 729 BP.
XX AC AAC35208;
XX DT 06-JUN-1993 (first entry)
XX DE Sequence encoding adenine phosphoribosyltransferase (apt).
XX KW Adenine phosphoribosyltransferase; probe; APRT activity; ss.
XX OS Arabidopsis thaliana.
XX PH Key Location/Qualifiers
XX FT 18..569
XX FT CDS /*tag= a
XX PN CA2069262-A.
XX PD 24-NOV-1992.
XX PF 22-MAY-1992; 92CA-2069262.
XX PR 23-MAY-1991; 91GB-0011126.
XX PA (UYNA-) UNIV WATERLOO.
XX PI Moffatt B;
```

```
XX WPI; 1993-053310/07.
DR P-PSDB; AAR30826.
XX PT Purified c DNA for apt. gene in plants - used for analysis of
PT adenine phosphoribosyl-transferase activity and function in plant
PT development
XX PS Claim 3; Fig 1; 27pp; English.
XX CC The apt cDNA of A. thaliana is described as a full-length clone.
CC However, the inventors cannot unequivocally rule out that there are
CC 5' sequences missing from this cDNA. The cDNA predicts a protein
CC molecular weight of 27,140.
XX SQ Sequence 729 BP; 204 A; 123 C; 188 G; 214 T; 0 other;

Query Match 20.0%; Score 88.2; DB 14; Length 729;
Best Local Similarity 56.0%; Pred. No. 2e-15;
Matches 181; Conservative 0; Mismatches 138; Indels 4; Gaps 3;

QY 115 GATCGCGCTTGGCGGATCGNCTCTNCATCCNGTNCATCCGACTTNCCAAAGCCA 174
DB 39 GATCCAGATCGCTAGATGGCTCTTCCATTAGACTCATCCCGACTTCCCTAAACCA 98
QY 175 GGGATNATGTTTCAGGACATCANGANGTNGTGTTCATCCCAAGCGNCTCCGTGACAAC 234
DB 99 GGAATCATGTTTTCAGGACATACGACGCTTCTTCGACACTGAGCGCTTTAAGGATACT 158
QY 235 ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNNTGAAATAGGAGTTAA 294
DB 159 ATTGCTTTTGTGTTAGATACAAAGATACAAAGGCATATCTGTTG--TTGCAGGTGTTGA 217
QY 295 AGCTAGAGGNTCANNTTTCGGAACAACACTANNCTTANAANNAATTTGTCAAAAATNGGTG 354
DB 218 AGCTAGAGGTTTCATTTTGGCCCTCTATTGCTTTG--GCTATTGTTGCCAAATTTGTT 275
QY 355 NCNATTCGGAAGCNAATNAGTNGCCANGCNAATGATTTTNGAANTANGAATTTTNG 414
DB 276 CCA--TGAGGAAGCCCAAGAGCTACCTGGAAGGTATTTCGGAGGAGTATTCGAGGAGTATTCGTTGGA 334
QY 415 GAATNNGGAATNNTAGATATAAA 437
DB 335 GTATGGAACAGATACGATTGAGA 357

RESULT 8
AAC40946
ID AAC40946 standard; DNA; 1036 BP.
XX AC AAC40946;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 30100.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
```

PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 04-MAY-1999; 99US-0132048.  
PR 05-MAY-1999; 99US-0132407.  
PR 06-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140911.  
PR 30-JUN-1999; 99US-0141297.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142134.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145065.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 26-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147269.  
PR 06-AUG-1999; 99US-0147416.  
PR 08-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0148171.  
PR 10-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 16-AUG-1999; 99US-0148684.  
PR 17-AUG-1999; 99US-0149368.  
PR 18-AUG-1999; 99US-0149175.  
PR 20-AUG-1999; 99US-0149222.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.

```

PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159320.
PR 14-OCT-1999; 99US-0159320.
PR 14-OCT-1999; 99US-0159321.
PR 14-OCT-1999; 99US-0159363.
PR 14-OCT-1999; 99US-0159368.
PR 18-OCT-1999; 99US-0159384.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match          19.7%; Score 86.8; DB 21; Length 1036;
Best Local Similarity 53.4%; Pred No. 5.9e-15;
Hatches 197; Conservative 0; Mismatches 168; Indels 4; Gaps 3;

Qy 69 CACCGGGCGCAGCGAGCGGGTGTGGCGATGGCTGCGTGGCTGATGGCTGGC 128
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 129 GGNATCGNCTCTNCAGTTCNCCGACTTNCAGGAGTTCGCAAGATGTCGCAAGATCC 334
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 335 TAAGATTCCTCTTCATAGTTCATCCCGACTTCCCTTAACAGGATCATGTTTCA 394
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 189 GGACATCANGANTGTTTTCGATCCAGCGGCTCCGTGACACATATACCATTTTGT 248
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 395 GCACATAACGACGCTTCTCTCGACACTGAGGCTTTAAGGATCTATTGCTTTGTTGT 454
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 249 CAAGCGGTACAGGACGACGAGNATCCACCTGGAANTAGAGTTAAAGCTAGAGGNTCA 308
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 455 TCATAGATACAAAGATAAAGCATATCTCTTG-TTGCAGGTGTTGAAGCTAGAGTTTCA 513
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 309 NTTTCGGAACACTANTNTCTTANAANAATTTGTCACAAAATNGTGNCNATTTAGGAGC 368
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 514 TTTTGGCCCTCTCTTCGTTG-GCTATTGGTCCAAATTTGTTCCCA-TGAGGACGC 570
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 369 NNAATNAGTCCGACGAAATGATTTTANCAATANGAATTTTNGGAATNNGAATNTT 428
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 571 CCAGAAGCTACCTGGGAGGTATTTCGGAGGAGTATTCTGTGGAGTATGGACCATTA 630
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 429 AGATAAAA 437
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 631 CGATTGACA 639
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
AAC33967
ID AAC33967 standard; DNA; 821 BP.
XX
XX AAC33967;
XX
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 4957.
XX
XX

```

```

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0125264.
PR 29-MAR-1999; 99US-0125785.
PR 01-APR-1999; 99US-0127452.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132663.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134222.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134769.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.

```

PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0158293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	22-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145210.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145216.	PR	22-OCT-1999;	99US-0160981.
PR	26-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147302.	PR	29-OCT-1999;	99US-0162142.
PR	05-AUG-1999;	99US-0147192.	Query Match 19.7%; Score 86.6; DB 21; Length 821;		
PR	05-AUG-1999;	99US-0147260.	Best Local Similarity 55.7%; Pred. No. 6e-15;		
PR	06-AUG-1999;	99US-0147303.	Matches 180; Conservative 0; Mismatches 139; Indels 4; Gaps 3;		
PR	06-AUG-1999;	99US-0147416.	QY	115	GATCGCGCTTGGCGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCACCAAGCCA 174
PR	09-AUG-1999;	99US-0147493.	Db	105	GATCCAGAAATCGCTAAGATTGCCCTTCCATTAGAGTCATCCCGACTTCCCTAAACCA 164
PR	09-AUG-1999;	99US-0147935.	QY	175	GGGATNATGTTTCAGACATCANGCNGTGTTCGATCCCAAGCGGNTCCGTGACAC 234
PR	10-AUG-1999;	99US-0148171.	Db	165	GGATCATGTTTCGGACATACGCGCTTCTTCGACACTGAGCGCTTAAAGGATACT 224
PR	11-AUG-1999;	99US-0148319.	QY	235	ATATACCAATTTCTCAACGGCTACAGGACCAAGNATCACCNTGGAAANTAGAGATTAA 294
PR	12-AUG-1999;	99US-0148341.	Db	225	ATTGCTTTGTTTGTGTATAGATACAAAGATAAAGGCATATCTGTG-TTGCAGGTGTGA 283
PR	13-AUG-1999;	99US-0148565.	QY	295	AGCTAGAGGNTCANITTTCCGGAACAACACTANNTCTTTANAANAATTTGTTCAAAATNSGTG 354
PR	13-AUG-1999;	99US-0148684.	Db	284	AGCTAGAGGTTTCATTTTGGCCCTCTCTATTGCGTTG--GCTATTGTTGCCAAATTTGTT 341
PR	16-AUG-1999;	99US-0149369.	QY	355	NCNATTCAGGAAGCNAATNAGNTGCCANGCNAATGATTTTNNANGAATANGAATTTTNG 414
PR	17-AUG-1999;	99US-0149179.	Db	342	CCCA-TGAGGAAGCCCAAGAGCTACCTGGGAAGGTTATTTTCGGAGAGATTTCCGTTGA 400
PR	18-AUG-1999;	99US-0149426.	QY	415	GAATNNGGAATNNTAGATAAAAA 437
PR	20-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	25-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151066.			
PR	27-AUG-1999;	99US-0151080.			
PR	30-AUG-1999;	99US-0151303.			
PR	31-AUG-1999;	99US-0151436.			

DB 401 GTATGGACAGATACGATTGAGA 423

RESULT 10  
AAC40942

ID AAC40942 standard; DNA: 780 BP.  
XX  
AC AAC40942;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 30085.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
XX  
PN EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130810.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134321.  
PR 14-MAY-1999; 99US-0134321.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138340.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0143977.  
PR 13-JUL-1999; 99US-0145542.  
PR 14-JUL-1999; 99US-0145624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.



PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139432.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140333.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144362.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145376.  
PR 27-JUL-1999; 99US-0145613.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.



```
Query Match          19.3%; Score 85; DB 21; Length 821;
Best Local Similarity 55.4%; Pred. No. 1.7e-14;
Matches 179; Conservative 0; Mismatches 140; Indels 4; Gaps 3;

Qy 115 GATGGCGCTTGGCGGNGATCGTCTTCCTCCATCCNGTGNATNCCGACCTNCCAAAGCCA 174
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 103 GATCCAGAAATCGCTAGATGCTCTTCCATAGAGTCATCCCGACCTTCCCTAAACCA 162

Qy 175 GGGATATGTTTCAGACATCANGANGTGTTCGATCCCAAGGCGTCCGTGACAC 234
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 163 GGAATCATGTTTCAGACATCAACGACCTTCCTCGACACTGAGGCTTTAAGGATCT 222

Qy 235 ATATACCATTTTCTCAAGCGGTACAGGACCAAGGATACACNTGGAANTAGGAGTTAA 294
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 ATGCTTGTTGTTGATAGATACAAAGATAAAAGCATATCTGTTG--TTGCAAGTCTTGA 281

Qy 295 AGCTAGAGGNTCANTTTTCGGAACAACACTANNTCTTANAANNAATTCGTCAAAAATNGGTG 354
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 282 AGCTAGAGGTTTCATTTTGGCCCTCCTATTGGGTTG--GCTATTGTCGCAAAATTTGTT 339

Qy 355 NCNATTGAGGAAGCNAATNAGTCCCAACNAATGATTTTNGAATANGAATTTTNG 414
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 340 CCCA--TGAGGACGCCCAAGAGTACCTGGRAGGTTATTTTCGGAGGATATTCGTTGGA 398

Qy 415 GAATNNGGAATNAGATAAAAAA 437
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 399 GTATGGACCATACGATGATTTGGA 421

RESULT 12
AAC43276
ID AAC43276 standard; DNA; 552 BP.
XX AC AAC43276;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38674.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123160.
XX PR 09-MAR-1999; 99US-0123348.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 08-APR-1999; 99US-0128234.
XX PR 16-APR-1999; 99US-0128714.
XX PR 19-APR-1999; 99US-0129845.
XX PR 21-APR-1999; 99US-0130077.
XX PR 23-APR-1999; 99US-0130449.
XX PR 28-APR-1999; 99US-0130510.
XX PR 30-APR-1999; 99US-0130891.
XX PR 04-MAY-1999; 99US-0131449.
XX PR 06-MAY-1999; 99US-0132048.
XX PR 08-MAY-1999; 99US-0132407.
XX PR 09-MAY-1999; 99US-0132484.
XX PR 09-MAY-1999; 99US-0132485.
XX PR 09-MAY-1999; 99US-0132486.
XX PR 09-MAY-1999; 99US-0132487.
XX PR 09-MAY-1999; 99US-0132863.
XX PR 09-MAY-1999; 99US-0134256.
XX PR 09-MAY-1999; 99US-0134218.
XX PR 14-MAY-1999; 99US-0134219.
XX PR 14-MAY-1999; 99US-0134221.
XX PR 14-MAY-1999; 99US-0134370.
XX PR 18-MAY-1999; 99US-0134768.
XX PR 19-MAY-1999; 99US-0134941.
XX PR 20-MAY-1999; 99US-0135124.
XX PR 21-MAY-1999; 99US-0135353.
XX PR 24-MAY-1999; 99US-0135629.
XX PR 25-MAY-1999; 99US-0136021.
XX PR 27-MAY-1999; 99US-0136392.
XX PR 28-MAY-1999; 99US-0136782.
XX PR 01-JUN-1999; 99US-0137222.
XX PR 03-JUN-1999; 99US-0137528.
XX PR 04-JUN-1999; 99US-0137502.
XX PR 07-JUN-1999; 99US-0137724.
XX PR 08-JUN-1999; 99US-0138094.
XX PR 10-JUN-1999; 99US-0138540.
XX PR 14-JUN-1999; 99US-0138847.
XX PR 16-JUN-1999; 99US-0139452.
XX PR 16-JUN-1999; 99US-0139453.
XX PR 17-JUN-1999; 99US-0139492.
XX PR 18-JUN-1999; 99US-0139454.
XX PR 18-JUN-1999; 99US-0139455.
XX PR 18-JUN-1999; 99US-0139456.
XX PR 18-JUN-1999; 99US-0139457.
XX PR 18-JUN-1999; 99US-0139458.
XX PR 18-JUN-1999; 99US-0139459.
XX PR 18-JUN-1999; 99US-0139460.
XX PR 18-JUN-1999; 99US-0139461.
XX PR 18-JUN-1999; 99US-0139462.
XX PR 18-JUN-1999; 99US-0139463.
XX PR 18-JUN-1999; 99US-0139750.
XX PR 18-JUN-1999; 99US-0139817.
XX PR 21-JUN-1999; 99US-0139817.
XX PR 22-JUN-1999; 99US-0139899.
XX PR 23-JUN-1999; 99US-0140353.
XX PR 23-JUN-1999; 99US-0140354.
XX PR 24-JUN-1999; 99US-0140695.
XX PR 28-JUN-1999; 99US-0140823.
XX PR 29-JUN-1999; 99US-0140991.
XX PR 30-JUN-1999; 99US-0141287.
XX PR 01-JUL-1999; 99US-0141842.
XX PR 02-JUL-1999; 99US-0142134.
XX PR 06-JUL-1999; 99US-0142055.
XX PR 06-JUL-1999; 99US-0142390.
XX PR 08-JUL-1999; 99US-0142803.
XX PR 09-JUL-1999; 99US-0142920.
XX PR 12-JUL-1999; 99US-0142977.
XX PR 13-JUL-1999; 99US-0143542.
XX PR 14-JUL-1999; 99US-0143624.
XX PR 15-JUL-1999; 99US-0144005.
XX PR 16-JUL-1999; 99US-0144085.
XX PR 16-JUL-1999; 99US-0144086.
XX PR 19-JUL-1999; 99US-0144325.
XX PR 19-JUL-1999; 99US-0144331.
XX PR 19-JUL-1999; 99US-0144332.
XX PR 19-JUL-1999; 99US-0144333.
XX PR 19-JUL-1999; 99US-0144334.
XX PR 19-JUL-1999; 99US-0144335.
XX PR 20-JUL-1999; 99US-0144352.
XX PR 20-JUL-1999; 99US-0144632.
XX PR 20-JUL-1999; 99US-0144884.
XX PR 21-JUL-1999; 99US-0144814.
XX PR 21-JUL-1999; 99US-0145086.
XX PR 21-JUL-1999; 99US-0145088.
XX PR 22-JUL-1999; 99US-0145085.
XX PR 22-JUL-1999; 99US-0145087.
XX PR 22-JUL-1999; 99US-0145089.
XX PR 22-JUL-1999; 99US-0145192.
XX PR 23-JUL-1999; 99US-0145145.
```



PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 21-MAY-1999; 99US-0135629.  
PR 24-MAY-1999; 99US-0136021.  
PR 25-MAY-1999; 99US-0136392.  
PR 27-MAY-1999; 99US-0136782.  
PR 28-MAY-1999; 99US-0137222.  
PR 01-JUN-1999; 99US-0137528.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138504.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 09-JUL-1999; 99US-0142977.  
PR 12-JUL-1999; 99US-0143542.  
PR 13-JUL-1999; 99US-0143624.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 99US-0144632.

PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.



[illegible]

XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX XX  
XX PD 06-SEP-2000.  
XX PF  
XX PP 25-FEB-2000; 2000EP-0301439.  
XX XX  
XX PR 25-FEB-1999; 99US-0121825.  
XX PR 05-MAR-1999; 99US-0123180.  
XX PR 09-MAR-1999; 99US-0123548.  
XX PR 23-MAR-1999; 99US-0125788.  
XX PR 25-MAR-1999; 99US-0126264.  
XX PR 29-MAR-1999; 99US-0126785.  
XX PR 01-APR-1999; 99US-0127462.  
XX PR 06-APR-1999; 99US-0128234.  
XX PR 08-APR-1999; 99US-0128714.  
XX PR 16-APR-1999; 99US-0129845.  
XX PR 19-APR-1999; 99US-0130077.  
XX PR 21-APR-1999; 99US-0130049.  
XX PR 23-APR-1999; 99US-0130510.  
XX PR 28-APR-1999; 99US-0130891.  
XX PR 30-APR-1999; 99US-0134421.  
XX PR 30-APR-1999; 99US-0132046.  
XX PR 04-MAY-1999; 99US-0132407.  
XX PR 05-MAY-1999; 99US-0132484.  
XX PR 06-MAY-1999; 99US-0132485.  
XX PR 06-MAY-1999; 99US-0132486.  
XX PR 07-MAY-1999; 99US-0132487.  
XX PR 11-MAY-1999; 99US-0132863.  
XX PR 14-MAY-1999; 99US-0134256.  
XX PR 14-MAY-1999; 99US-0134218.  
XX PR 14-MAY-1999; 99US-0134219.  
XX PR 14-MAY-1999; 99US-0134221.  
XX PR 14-MAY-1999; 99US-0134370.  
XX PR 18-MAY-1999; 99US-0134768.  
XX PR 19-MAY-1999; 99US-0134941.  
XX PR 20-MAY-1999; 99US-0135124.  
XX PR 21-MAY-1999; 99US-0135353.  
XX PR 24-MAY-1999; 99US-0135629.  
XX PR 25-MAY-1999; 99US-0136021.  
XX PR 27-MAY-1999; 99US-0136392.  
XX PR 28-MAY-1999; 99US-0136782.  
XX PR 01-JUN-1999; 99US-0137222.  
XX PR 03-JUN-1999; 99US-0137528.  
XX PR 04-JUN-1999; 99US-0137502.  
XX PR 07-JUN-1999; 99US-0137724.  
XX PR 08-JUN-1999; 99US-0138094.  
XX PR 10-JUN-1999; 99US-0138540.  
XX PR 10-JUN-1999; 99US-0138847.  
XX PR 14-JUN-1999; 99US-0139119.  
XX PR 16-JUN-1999; 99US-0139452.  
XX PR 16-JUN-1999; 99US-0139453.  
XX PR 17-JUN-1999; 99US-0139492.  
XX PR 18-JUN-1999; 99US-0139454.  
XX PR 18-JUN-1999; 99US-0139455.  
XX PR 18-JUN-1999; 99US-0139456.  
XX PR 18-JUN-1999; 99US-0139457.  
XX PR 18-JUN-1999; 99US-0139458.  
XX PR 18-JUN-1999; 99US-0139459.  
XX PR 18-JUN-1999; 99US-0139460.  
XX PR 18-JUN-1999; 99US-0139461.  
XX PR 18-JUN-1999; 99US-0139462.  
XX PR 18-JUN-1999; 99US-0139463.  
XX PR 18-JUN-1999; 99US-0139750.  
XX PR 18-JUN-1999; 99US-0139763.  
XX PR 21-JUN-1999; 99US-0139817.  
XX PR 22-JUN-1999; 99US-0139899.  
XX PR 23-JUN-1999; 99US-0140353.  
XX PR 23-JUN-1999; 99US-0140354.  
XX PR 24-JUN-1999; 99US-0140695.  
XX PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142134.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.







GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 01:36:02 ; Search time 2691 Seconds  
(without alignments)  
4758.541 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 440  
Sequence: 1 cgtccgcgcgcgcgaattc.....ggaaatnntagataaaaaant 440

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_em.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pin.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	4.5	128875	2	AC129615
C 2	19	4.3	10525	1	AE012058
C 3	19	4.3	126259	1	AC078977
C 4	19	4.3	139468	8	AC090441
C 5	19	4.3	175439	8	AP001111
C 6	18	4.1	10144	1	AF011676
C 7	18	4.1	10527	1	AF028006
C 8	18	4.1	10895	1	AE012522
C 9	18	4.1	11903	1	AE011785
C 10	18	4.1	36690	2	AC014124
C 11	18	4.1	82815	2	AC062001
C 12	18	4.1	86896	1	RCU57682
C 13	18	4.1	104802	9	AP003026
C 14	18	4.1	110000	2	LMFICHR31_13
C 15	18	4.1	110000	2	LMFICHR32_21
C 16	18	4.1	113856	8	AC108883
C 17	18	4.1	124253	2	AP003990
C 18	18	4.1	130451	2	AP004000
C 19	18	4.1	131197	2	OSJN00216
C 20	18	4.1	142381	8	AC079632
C 21	18	4.1	143549	2	AC118287
C 22	18	4.1	144890	2	AP005528
C 23	18	4.1	150153	2	AC091869
C 24	18	4.1	150927	2	AP004756
C 25	18	4.1	153137	2	AC117088
C 26	18	4.1	159079	2	AP005197
C 27	18	4.1	160301	3	AC007413
C 28	18	4.1	162342	2	AP004687
C 29	18	4.1	164518	2	OSJN00128
C 30	18	4.1	166854	3	AC007330
C 31	18	4.1	166885	9	AC091873
C 32	18	4.1	172864	2	AC109452
C 33	18	4.1	173555	8	AP003277
C 34	18	4.1	176199	2	AP005316
C 35	18	4.1	187835	8	AP002482
C 36	18	4.1	187916	2	AP003458
C 37	18	4.1	188635	2	AC011207
C 38	18	4.1	192516	2	AC074206
C 39	18	4.1	198818	2	AC107768
C 40	18	4.1	201642	2	AP005529
C 41	18	4.1	203952	10	AL645764
C 42	18	4.1	212050	1	AL646060
C 43	18	4.1	213140	10	AC092480
C 44	18	4.1	275390	3	AE003831
C 45	18	4.1	345783	1	AP003001

ALIGNMENTS

RESULT 1  
AC129615/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AC129615 128875 bp DNA linear HTG 24-AUG-2002  
Rattus norvegicus clone CH230-430L22, \*\*\* SEQUENCING IN PROGRESS  
\*\*\* 43 unordered pieces.

AC129615  
AC129615.1 GI:22024298  
HTG; HTGS\_PHASE1.  
Norway rat.

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 128875)  
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, C., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hernandez, J., Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulys, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Louisegh, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mavhiney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackemele, O., Okwuonu, G., Olarunpago, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzoi, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, F., Rojas, A., Rose, K., Rose, K., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shacsmen, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, D., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, X., Yen, J., Yoon, V., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

Consensus quality: 95541 bases at least Q30  
 Consensus quality: 98821 bases at least Q40  
 Consensus quality: 100748 bases at least Q20

NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 NOTE: This is a "working draft" sequence. It currently  
 consists of 43 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1025: contig of 1025 bp in length  
 1125: gap of unknown length  
 1126: contig of 1261 bp in length  
 2385: gap of unknown length  
 2487: contig of 1298 bp in length  
 3785: gap of unknown length  
 3885: contig of 1133 bp in length  
 5017: gap of unknown length  
 5117: contig of 1715 bp in length  
 6832: gap of unknown length  
 6933: contig of 1493 bp in length  
 8425: gap of unknown length  
 8525: contig of 1366 bp in length  
 8526: gap of unknown length  
 8826: contig of 1188 bp in length  
 9992: contig of 1847 bp in length  
 11179: gap of unknown length  
 11273: contig of 1503 bp in length  
 13126: gap of unknown length  
 13227: contig of 1183 bp in length  
 14829: gap of unknown length  
 16012: contig of 1183 bp in length  
 16112: gap of unknown length  
 17249: contig of 1137 bp in length  
 17349: gap of unknown length  
 17350: contig of 2219 bp in length  
 19568: gap of unknown length  
 19569: contig of 1608 bp in length  
 21276: gap of unknown length  
 21377: contig of 1144 bp in length  
 22520: gap of unknown length  
 22620: contig of 2150 bp in length  
 24770: gap of unknown length  
 24870: contig of 1703 bp in length  
 26573: gap of unknown length  
 26573: contig of 1776 bp in length  
 28449: gap of unknown length  
 28549: contig of 2269 bp in length  
 30818: gap of unknown length  
 30918: contig of 2200 bp in length  
 33118: gap of unknown length  
 33218: contig of 2003 bp in length  
 35221: gap of unknown length  
 35321: contig of 2416 bp in length  
 37337: gap of unknown length  
 37837: contig of 2216 bp in length  
 40053: gap of unknown length  
 40153: contig of 2132 bp in length  
 42285: gap of unknown length  
 42385: contig of 2612 bp in length  
 44997: gap of unknown length  
 45097: contig of 2725 bp in length  
 47822: gap of unknown length  
 47922: contig of 3131 bp in length  
 51053: gap of unknown length  
 51153: contig of 2566 bp in length  
 53719: gap of unknown length  
 53819: contig of 2095 bp in length  
 55914: gap of unknown length  
 55915: contig of 2319 bp in length  
 56015: contig of 2319 bp in length

## COMMENT

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: KBZR

Center clone name: CH230-430L22

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: version 0.990329

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

differing host specificities  
Nature 417 (6887), 459-463 (2002)  
12022145  
2 (bases 1 to 10525)  
da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,  
Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida  
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,  
Chamargo, F., Ciapina, L.P., Ciccarelli, R.M.B., Coutinho, L.L.,  
Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S.,  
Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C.,  
Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite  
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locati, E.C., Machado, M.A.,  
Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.,  
Mench, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M.,  
Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,  
Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F.,  
Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos  
Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and  
Kitajima, J.P.  
Direct Submission  
Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de  
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,  
Brazil

## FEATURES

Location/Qualifiers  
1..10525

source

/organism="Xanthomonas axonopodis pv. citri str. 306"  
/strain="306"  
/db\_xref="taxon:190486"  
/note="pathovar: citri"  
complement(344..1075)  
/gene="fabG"  
/note="XAC4090"  
complement(344..1075)  
/gene="fabG"  
note="identified by sequence similarity; putative; ORF  
located using Blastx/Glimmer/Genemark"  
/codon\_start=1  
/transl\_table=11  
/product="3-oxoacyl-[ACP] reductase"  
/protein\_id="AA38925.1"  
/db\_xref="GI:21110508"  
/translation="MNSARRALVTGGDGLGGAICRHLAAQGRHVIVHANGNLRAD  
EVAALVADGGSAQAVFDVADQAASSAALSLEAGPIQIVVNNAGTHDDAPMAGN  
VEQHRVIDVSLHGFNFVPTPLIPMARTGRVGVSVSSVAALVNGQTQYAAAKAA  
LHGAKSLSRMASRGIAVNVAPGVIESDMVGDGFAPEAKOLVPAGRVGPDEVA  
LVAFCLSDAAGVINGQVINGCMG"  
1258..1806  
/gene="XAC4091"  
1258..1806  
/gene="XAC4091"  
note="putative; ORF located using Glimmer/Genemark"  
/codon\_start=1  
/transl\_table=11  
/product="hypothetical protein"  
/protein\_id="AA38926.1"  
/db\_xref="GI:21110509"  
/translation="MSAANLAGIKQGEDAMNWLQHGFSYVAICQADPTAPLFGT  
AVKRPDLLESLIGLIAIDVKNVQFKHQAQCYSLPYSELKRAVAFERLFRIPYV  
YAYNRDAGRSPHWTLSAKALEVGEIKPARDNDPEFLSIGLEHFEHVSGGDIARLY  
THRPLSVANLSALVASKTPAAS"  
complement(1815..2351)  
/gene="XAC4092"  
complement(1815..2351)  
/gene="XAC4092"  
note="identified by sequence similarity; putative; ORF  
located using Blastx/Glimmer/Genemark"  
/codon\_start=1  
/transl\_table=11  
/product="phosphotransferase"  
/protein\_id="AA38927.1"  
/db\_xref="GI:21110510"

gene

CDS

Query Match 4.5%; Score 20; DB 2; Length 128875;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 75 CGGCAGCGGAGGCGGCGG 94

Db 5568 CGGCAGCGGAGGCGGCGG 5549

## RESULT 2

AE012058 Xanthomonas axonopodis pv. citri str. 306, linear BCT 29-MAY-2002

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of

AE012058 Xanthomonas axonopodis pv. citri str. 306, section 436 of 469 of







```

/protein_id="BAA90493.1"
/db_xref="GI:8099121"
/translation="MKDRAYSHVNHKFKKNAAGRHDRQARPPQPPASPPDG
KRRKRRRGGRGVEGMRKVRKRSERERVKRVGVC"
join(19740..19772,19782..20585)
/notes="similar to an Arabidopsis thaliana chromosome BAC
genomic sequence; unknown protein (AC005896)"
/codon_start=1
/protein_id="BAA90494.1"
/db_xref="GI:8099122"
/translation="MAALLQRLVVDPGAPWFREFVLGMLKFKVAATAVAMAVALS
ETORLGEEMLYAMARAFQLSGVIGVFIQFTQKSAWILLAYLFMYTVAGYTAGO
RANRYPGNHIAASVLAGTSVMMALIVARFPPTPRYIIPVAGMMVGNMAYTVCVT
MKKREDGQGVETALGATPGOATQRVRSVLIALSPVIDNAKTVGLIALPG
AMTLIMGASPLEIAIQIIVYNNMLGASTVSSILTYLCWPAFTTGAFOLNDAVEA
AD"
complement(join(23510..23881,24027..24188))
/codon_start=1
/product="hypothetical protein"
/protein_id="BAA90495.1"
/db_xref="GI:8099123"
/translation="NEKDKGLVSNLMHGVAGGHAYPYPOQGYPPPTIAYPPPGY
AAYQGYMSIVMEVAMVEECTWELRCLRVQSPRPRTVHISFLPMAAMEATVTVAVT
MAVASIAATWATAITANTMEATIDTITITMAASMAVIDTITATTAAASNAVITAVTM
VATINWALSFSCLLNK"
complement(join(24811..25139,25263..25275))
/codon_start=1
/product="hypothetical protein"
/protein_id="BAA90496.1"
/db_xref="GI:8099124"
/translation="MPINITRVPSSLVPLSLPLRACLMLHGCSAKPROWRRSRAVV
QHRHRCPPINAAPRSRPSTVPGVRLAKHHRDGPRAASVYHREKRKRKEKGR
REKNFWSST"
complement(join(27825..28114,28880..29102))
/notes="rice EST C27893 corresponds to a region of the
predicated gene: unknown protein"
/codon_start=1
/protein_id="BAA90497.1"
/db_xref="GI:8099125"
/translation="MGCSDEQDRLGFLSNLMHGVAGGGGGHYPPYPOQGYPPPT
AYPPPPYGGYGTFPAGTGGSAFFPGHNGHGGNMGLAAGAAAAYGAHLS
GGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGH
GGHGGHGGH"
complement(join(30818..31009,31659..31892))
/notes="rice ESTs AW54121, AW155454, D48581 correspond to
a region of the predicated gene; unknown protein"
/codon_start=1
/protein_id="BAA90498.1"
/db_xref="GI:8099126"
/translation="MGILLTRDTLLRATRRRERTRLLGLIPLLLGLTLHLGLTLLH
SMGTLSLVATLHLVTPNMVATLLRATPDHLGTIRISHGGHGMGYGGHGGFGTGHG
YGGHGGKPKHGKHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGHGGH
join(32858..33002,33787..33957)
/codon_start=1
/product="hypothetical protein"
/protein_id="BAA90499.1"
/db_xref="GI:8099127"
/translation="METRVERESASWKRKNKGAQAOKRTDGGCGPSVTLVRG
SNNGEAREGARDSRAVAGRWKSRFPSCATASFPLPLRWVKS"
complement(join(34443..34457,34764..35338,38598..38691))
/notes="similar to an Arabidopsis thaliana chromosome BAC
genomic sequence; unknown protein (AC006592)"
/codon_start=1
/protein_id="BAA90500.1"
/db_xref="GI:8099128"
/translation="MLQRAASNAVSWWASHIRTKQSKWLDNLDHQSLLIEDIKLI
DYVMENASPLEEFKFORADIALEENCFWMKFTSQQLGGFTKYEQLOPEIGKIT
NKDLKTNNGRADPSKAGSNIAKRLKLEIQLQWLEONAMLGELQYRFASLCS
IQKELPATMGGADPEGAFTSYQAQAFQGVENMKQENNVKVADELQSLDHIKGLQ
AELEKAPWN"
join(40709..40902,41984..42310,43605..43608)
/notes="similar to a putative RING zinc finger protein of
Arabidopsis thaliana (AC003672)"

```

```

/codon_start=1
/protein_id="BAA90501.1"
/db_xref="GI:8099129"
/translation="MEDAAQASREWDGGGGGGGADAVLAGAGASLSLCYHFAFGP
HDELLERAUULLPDLLQGRFGTKVDKFKAGCSWLSDERVLCIQFARRALGAGMKLE
NFMGKWRSPSGMRADQLMEGEVCEKLAGTETWVHAFSVADLPLAFADRAALFOE
RPKWRKDLQPYIR"
complement(join(44354..46675,46865..47167,47197..47259))
/notes="maize EST AI621709, similar to an Arabidopsis
thaliana chromosome BAC genomic sequence (AC006193)"
/unknown protein"
/codon_start=1
/protein_id="BAA90502.1"
/db_xref="GI:8099130"
/translation="MRLATSLIWCARESQLMASPIGRSPSTPSSNHRPSTPSI
HRPSTGATRSIGTSTPSPRSNNGVGGGGGGKSEPNPSPATAPRLUSDPSFR
SVDSKPVVERVPKICPPPKQPRKAEALQARLESAGEDLKKAKQLAFAPVGERDLV
GELNEAKRVADETHEKLDALMAKMAWEATEIEKFRADELQAGIQIDQAREEWOR
EILCSVGHAAADLLVLTTEELRFRRLAMANEAKKALGADDAMKIAVNEAKY
EILSVSVRLAGLDDTAESSEKRNTEIIVNLESEVSVLKGLKEARLIEERLAE
TEKLEIKSEVADAKAESEARQLFEEMKHKAGLLEMELEAVTLDKFKGESLASTT
EELGQSALDQRESEIEVLKQTLTLEIVARLLADVNESEQFDSAQOOFQLQTT
DLYRNKLEAEAEASALNNEKAANKIEGLTEENYKLISELNTRDREKRAVE
DIAALSEESKAKAEHARYLSKEDDHEHALAQIGDKWALKSTRESEYVMDLEAND
ITCLRNVDLKAEVNYRRECEKETIDVRLNKQSEETISALQLEVQKAVESLODAE
HQQVANEKEKLOERLVYTESACAEASKALHEAKTESLEKLIYTEAAVAEANKS
VOEATYNSOLKERLIDKNAQLSQTQENDEFRLREADAMKKIDELSALLAEAMIKH
PEEEKLVVDEAYSSVHREVTDVSVENGDAESNDKNPKLELDVLRSSNGDMHEE
EKGETKRVQEVKTECTOESNKILKQHPDPKQETVSKDELEPENTYHPNGT
VSDTSKQVMSPTTPOQOKKNKPLLKEGSLKKKNSK"
join(47609..47900,52420..52836)
/codon_start=1
/product="hypothetical protein"
/protein_id="BAA90503.1"
/db_xref="GI:8099131"
/translation="MAEEEEERTLHTSLFALORRRRRREREAMAPLRKLQROKA
NKGREGEGAGKRRHMPKTKMDDATTITATVTTSSGSGGERLAKLAVYGRG
ARWSTVHPGKTWSIGRTQELVGLRIQRCPCWCCVDEELSCGHAGEDLAGHN
ARMEETALDLSRGCIPIVHDTWEELVGLRLHARALSPLAGQRGRSSQTCGAQRGG
GGSLTATRVGRNLLADK"
complement(join(55588..55792,56227..56309))
/codon_start=1
/product="hypothetical protein"
/protein_id="BAA90504.1"
/db_xref="GI:8099132"
/translation="MASAGYFAGGVKRVAVRFDGKRPAGRADVFSHHRHRLMY
SLLVREERORRKEVSEGTGACTAAAVRRSGGGGAAQRGGAAGAAA"
join(57355..57465,57473..57754,58048..58056)
/codon_start=1
/product="hypothetical protein"
/protein_id="BAA90505.1"
/db_xref="GI:8099133"
/translation="MLCTEHLIAATAVTYNARGODENTGTDEAAAAYGEVAITEIVK
ERAGDVEERQLRSDVEIGREIAAAGRGKRCGRKGPSSSLTLRSCWNSRYERA
ELTLLMLQLQPCVPVAGCTPHPRVAHLTRDI"
59272..59714
/codon_start=1
/join(60723..60890,62174..62417,63196..63584)
/notes="similar to orf5, rice gypsy-type retrotransposon
RIR2 (AB030283)"
/codon_start=1
/protein_id="BAA90506.1"
/db_xref="GI:8099134"
/translation="MAERESFESQAPSDVTEDNLKEMAHVLPKAEITIGWRPAFG
EAPTPDTHEDVADNVPSEDPPTVSQACAGVQHQPSTENQSGDSQKTPVEVE
AOTSPPKKAGNDSETPVTRSPRGITDRTKSAQDFVLVGKTKLLEGA
WTEVAANAAPLIVAMFNNNGSALDASEIFDKLRVADIPFKNIKAGSIGASLALA
MTKSLPVDVDAIDGDTSEAAALDLISDAOKATDKIADVVVERF"
complement(join(66031..66576,67753..67820,68025..68234,
68364..68445,68871..69010,69024..70098))
/notes="similar to prpol, rice retrotransposon (AB030283)"
/codon_start=1
/join(70145..70587)

```

CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

LTR

CDS

CDS

CDS

LTR

CDS	complement(join(72094..72112,72191..74136)) /note="similar to ABC transporter of Arabidopsis thaliana (AC004697)" /codon_start=1		gene
CDS	Query Match 4.3%; Score 19; DB 8; Length 175439; Best Local Similarity 100.0%; Pred. No. 21; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		gene
QY	90 GCGCGTGGCGCGATGGCG 108       	10144 bp DNA linear BCT 29-MAY-2002	CDS
Db	19850 GCGCGTGGCGCGATGGCG 19868		
RESULT 6	AE011676 10144 bp DNA linear BCT 29-MAY-2002		gene
LOCUS	Xanthomonas axonopodis pv. citri str. 306, section 54 of 469 of the complete genome.		CDS
DEFINITION	AE011676 AE008923		
ACCESSION	AE011676.1 GI:21106580		
VERSION			
KEYWORDS			
SOURCE	Xanthomonas axonopodis pv. citri str. 306.		
ORGANISM	Xanthomonas axonopodis pv. citri str. 306 Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xanthomonas.		
REFERENCE	1 (bases 1 to 10144)		
AUTHORS	da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J., Chambergo,F., Clapina,L.P., Ciccarelli,R.M.B., Coutinho,L.L., Cursino-Santos,J.R., El-Dorri,H., Faria,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locall,E.C., Machado,M.A., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J., Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P.		gene
TITLE	Comparison of the genomes of two Xanthomonas pathogens with differing host specificities		CDS
JOURNAL	nature 417 (6887), 459-463 (2002)		
MEDLINE	22022145		
PUBMED	12024217		
REFERENCE	2 (bases 1 to 10144)		
AUTHORS	da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J., Chambergo,F., Clapina,L.P., Ciccarelli,R.M.B., Coutinho,L.L., Cursino-Santos,J.R., El-Dorri,H., Faria,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locall,E.C., Machado,M.A., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J., Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P.		gene
TITLE	Direct Submission		CDS
JOURNAL	Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900, Brazil		
FEATURES	Location/Qualifiers 1..10144 /organism="Xanthomonas axonopodis pv. citri str. 306" /strain="306"		
SOURCE			



```

/protein_id="AAM35385.1"
/db_xref="GI:21106584"
/translation="MFAGNHAMGEAHLFVIGTLLAWLGRVYLVFVGVLGLGWLMI
DPDLPAHQSWWVLTSGALVAFEDTADIPGVDSGDWDLDTLQARVPAQAFIAAATL
SPDQDGLGAAGAGVALTSHTLKAGTRALINTSPEPASNWIASLADDTATTALAL
ALAHPLWALGLAVGSSLMAGLVVWVWRLNRLLGRMRULVAPTRPAATPTARSSLP"
6233..6817
/gene="XAC0497"
CDS
6233..6817
/gene="XAC0497"
/feature="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM35386.1"
/db_xref="GI:21106585"
/translation="MKAPALQQAQRQVQRRQIEQLQQRQVNLAMSDKISRANNE
VQASLAREDEQTAALRADVAFYERLVGSTAQRKGLNARSVQFTAEAGGTGVSVLQ
NLNRAISQQLRFQAVEGVRAKGLVTVSNWELHOKPDAAAGOPYSEFYQLQDGSVILP
KDFTPQVRKVISLSDGAPVQSOTFDMKRVAGNGAGE"
6821..7270
/gene="XAC0498"
CDS
6821..7270
/gene="XAC0498"
/feature="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM35387.1"
/db_xref="GI:21106586"
/translation="MFGNKSRRGAGOTVDTLIGPOVYIRGDLTFSGGLYVGRILGV
IAEDQAGNLTVAEGSTEGEVRAPVYIINGQLTGDVHAARVELAANRVOGNVHIQ
WEMSAQNLTLGRLHTATTAGATNALPAPEPSRAEPVTLQNETADA"
7354..7740
/gene="XAC0499"
CDS
7354..7740
/gene="XAC0499"
/feature="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM35388.1"
/db_xref="GI:21106587"
/translation="NSTLVSLPTAAPADPYQSIDRPLNFSVAAAARVRELIQESGNA
LALRVYIGGSGSGQYGFEDENRAEDDLAVATDVTLLVDPLSLQLYLMGAEDVYTE
SLTGAQFVIRNPNAKTTGCGSSFSV"
complement(8092..8589)
/gene="XAC0500"
CDS
complement(8092..8589)
/gene="XAC0500"
/feature="putative; ORF located using Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAM35389.1"
/db_xref="GI:21106588"
/translation="MYTARRIGIDTRHGRVSTVSHMTAVDQRQAAVGENAHIVAP
AEARTQGHLDPTTANARSRRRETCSAESVVARHARVQVAGLAGATQAIRCPVAH
HRQPATRCIPVWALKIATAPRAAQALSTRVRDCLRVTTWRAAVTVLKDCRRIAQRGS
THTPA"
8789..9946
/gene="XAC0501"
CDS
8789..9946
/gene="XAC0501"
/feature="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1

```

Query Match 4.18; Score 18; DB 1; Length 10144;  
 Best Local Similarity 100.08; Pred. No. 65;

```

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 89 AGCGCGTGTGGCGATGG 106
Db 5489 AGCGCGTGTGGCGATGG 5506

RESULT 7
LOCUS AF028006/c
DEFINITION AF028006 10527 bp DNA linear BCT 07-JAN-1998
Methanosarcina barkeri atp operon: ATP synthase beta subunit
(atpB), ATP synthase epsilon subunit (atpE), ATP synthase gene 1
(atpI), ATP synthase alpha subunit (atpA), ATP synthase gamma subunit
(atpG), ATP synthase delta subunit (atpD), ATP synthase alpha subunit
(atpA), ATP synthase gamma subunit N-terminus homolog (atpG), and
ATP synthase gamma subunit C-terminus homolog (atpI) genes,
complete cds.
ACCESSION AF028006
VERSION AF028006.1 GI:2605818
KEYWORDS Methanosarcina barkeri.
SOURCE Methanosarcina barkeri.
ORGANISM Methanosarcinaceae; Methanosarcina.
REFERENCE 1 (bases 1 to 10527)
AUTHORS Sumi, M., Yoshida, M., Koga, Y. and Yoshida, M.
TITLE F0P1-ATPase genes from an archaeobacterium, Methanosarcina barkeri
JOURNAL Biochem. Biophys. Res. Commun. 241 (2), 427-433 (1997)
MEDLINE 98086367
PubMed 9425287
REFERENCE 2 (bases 1 to 10527)
AUTHORS Sumi, M., Yoshida, M., Koga, Y. and Yoshida, M.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1997) The Research Laboratory for Resources
Utilization, Tokyo Institute of Technology, 4259 Nagatsuta,
Midori-Ku, Yokohama, Kanagawa 226, Japan
FEATURES
Source
1..10527
/organism="Methanosarcina barkeri"
/strain="MS (DSM 800)"
/db_xref="taxon:2208"
/note="atp operon"
2243..3652
/gene="atpB"
2243..3652
/gene="atpD"
/codon_start=1
/transl_table=11
/product="ATP synthase beta subunit"
/protein_id="AAC38049.1"
/db_xref="GI:2605819"
/translation="MVDSRLNLGKLVISVGRSIVDLFEKHLPPVTLIAGRESOI
ALEVTLQDAHHVGLAIAITPEGLARGMAVEOTGGPKAPWGSEILLRSMFVQNTID
RRPSPDILQWRSIHOTPEPLMRSTSEIFETGIRADIVLPLERGGKAGLPGAGVG
KVLLEIMHNVYHQGVISFCIGIGEREGEELIRDMKADGVLNPTVYFGQNEF
PGARFVRGHTALMAEYFDDRDVLLIDNIFRFGIQAQSEVSLGMSQVPSRLGTOP
TIGTSELIERISTTDAGAIMSQAQVYVADDETPPSAVHTFSLSIASIVLSKRAS
EGLYPAIDPLQSNKMATPGIVGRHYLLAQEIQTQLAQVSELKDIISMLGLEQSP
DNVVARARLERFLTPFFFTTEGTGKGSISLSDALDGCERILNDEFKDYSEGDL
YMGITIDEMAKKSSREKS"
3649..4083
/gene="atpC"
3649..4083
/gene="atpC"
/codon_start=1
/transl_table=11
/product="ATP synthase epsilon subunit"
/protein_id="AAC38050.1"
/db_xref="GI:2605820"
/translation="MNSGLMNSGLMNSGLMNSLNTILLPFQVFAKKGVSRIVAGREGS
FGLPRLDCVATLPGILTYETESEGEVYVAVDEGLIKNGQYVLVSVRDAIFDTDL
SOLHEAVEKFLTLDTEQKIRSVYVVKLETGLIRLRAEQNV"
4076..4414
/gene

```

```
/gene="atpi"
4076..4414
/gene="atpi"
/codon_start=1
/transl_table=11
/product="ATP synthase gene 1"
/protein_id="AAC38051.1"
/db_xref="GI:2605821"
/transl_table="MSDKPSKPLEDESFLARQVGTKAERKIAQRAHVDRTINILGLM
MGLIGWAVAPTLIGAALGWLMDKHPESFWALTMLILGLITGLNAHWHLAKERQE
MOREEDYNE"
4407..4721
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AAC38052.1"
/db_xref="GI:2605822"
/transl_table="MNELLNLFSLTAGLGVFGGLGMMVTVQKLSRKPATWFLG
SLIRLSIVAGFVSDGYWERLLICLGFVWRHRIIVLTRLPEEDPNQLTREASN
AT"
4711..5283
/gene="atpB"
4711..5283
/gene="atpB"
/codon_start=1
/transl_table=11
/product="ATP synthase a subunit"
/protein_id="AAC38053.1"
/db_xref="GI:2605823"
/transl_table="MRLSPDELFWQDFIKINATIVTWGLMLVMVIGSKTITSKLS
TGLSRKWNILEIVAGLFOEDYGLQPKKILGELGTLFLFIANVLICILPGYE
PPTGSUSTARALCLVFNVPFLGIEQGISYLYKTYTEPTIIMLPFNIEISRTLA
LAIRLFGNMGSMIVAILLITPTFFILIL"
5437..5712
/gene="atpE"
5437..5712
/gene="atpE"
/codon_start=1
/transl_table=11
/product="ATP synthase c subunit"
/protein_id="AAC38054.1"
/db_xref="GI:2605824"
/transl_table="NALQTYITTTAVASATSGITIGVIGPAIGRAVATALSSL
AQCPDASANTRTFLVGLAMIESLATYCFVSMILIFANPWNRLT"
5733..6893
/gene="atpF"
5733..6893
/gene="atpF"
/codon_start=1
/transl_table=11
/product="ATP synthase b subunit"
/protein_id="AAC38055.1"
/db_xref="GI:2605825"
/transl_table="MLIDMTVIAQVINFLILWLLKFLVKPLNADARENKVANE
LKNADAEAKQKEKEEFKRNKEEDQORNDLLNKAKEEAQERQAFEDVFEASLYL
RAKQAEALNEGONISQEQROTQOEVFSTARKILDTLTSELRADVDFVQERLNL
QDNKKOLASALSTSPGOVLRTAFDLPQTDQSDIKKAIKETLDTQPRFTLPDLV
SGIELNTDQGVASADYLTSMQKSIDELLNQPKSEKSEFQTKNNKAKTEPQTKN
NKPFEPAEQELEAETNEPRKTESVKTTPATEYNPNRKSKELETQEEDAKOE
SEARQEDAKQSEAKQSEAOEMPDQAKQSEAKQSEVKKQSGNSPNLWR"
6890..8636
/gene="atpA"
6890..8636
/gene="atpA"
/codon_start=1
/transl_table=11
/product="ATP synthase alpha subunit"
/protein_id="AAC38056.1"
/db_xref="GI:2605826"
/transl_table="MRLIPNSPKPEVNNMETKSLDKVDKVFTEIHQVRESVPTLT
PREVCRILTYSTGIANVSGLTGVGDELIFPGDLFGIAFNWDEKEIGTVLLGEYSHL
HAGQOQVTRVRMDVAVGELLGRVIDPLGRPLDNKGPTVSKRLPIERPSPAIMDRA
PYTPYLTQGVKVIDALIPIGRGQRELILDRQGTAKTAIDTILNQRNENVLVCYCAI
```

```
GORASAVANLRRERGAMDYTIWVTEGNDPSGLIYITPYAATSIAYEFMESGRDV
LIYDDLTNARAVRELSLLRRRPGREAYPGDIFYIHSRLLRSTHLLKEFGGSLT
ALPIIETEAONISAYIPTNLISITDGOYILSPSLFELGVLAVDVGKSVRGGAQL
AAYREVAGDLKAYSOFELETFPRGAKIDENTRRELIHGRRIRALLKQPHNSVPV
PQOIVILVALNKLFDNPLDKMVEANSILKALPIDEDVREKFGDKELSKDRET
ILNIARKALEPYQPKPESSEKPEAKTEANESSTOTEDKSEAKTEEKVAKSETQTK
GPETETETEEKPEFGTRTEEK"
8712..9161
/gene="atpG"
8712..9161
/gene="atpG"
/codon_start=1
/transl_table=11
/product="ATP synthase gamma subunit N-terminus homolog"
/protein_id="AAC38057.1"
/db_xref="GI:2605827"
/transl_table="MTTETQSRLTKIDRAKDLQSVVTRMKALAAASNIGQEKVSALS
DYVYVEGLGLCPKTAEMPAQSGKRAOKNTRLIGAVVFGSDOGLVQGFNDIITDYA
VRELKAPGKAOVWANGELVIHAWKMKARLLDFIMCQIRLRQLPRL"
9056..9616
/gene="atpJ"
9056..9616
/gene="atpJ"
/codon_start=1
/transl_table=11
/product="ATP synthase gamma subunit C-terminus homolog"
/protein_id="AAC38058.1"
/db_xref="GI:2605828"
/transl_table="MGCGRACYSRLEDEGLPLGLYNVPSVKATPPLIAQILVENEK
LRQSDDEALHYLNHRKTVTEPVQSRLPDEPDETWRDRLTKSWPTKLLPEVNGK
ITITRALIRFVLSVFRACAEASLSESSRLAANQRAKADNIEELNSLGSYYVR
OSQIDELFEVVSQGFALSRAKSSRR"
BASE COUNT 3157 a 2133 c 2435 g 2802 t
ORIGIN

Query Match 4.1% Score 18; DB 1; Length 10527;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 238 TACCATTGTCACAGCGG 255
|||||
DB 8311 TACCATTGTCACAGCGG 8294

RESULT 8
AE012522
LOCUS
DEFINITION
Xanthomonas campestris pv. campestris str. ATCC 33913, section 430
of 460 of the complete genome.
ACCESSION
AE012522 AE008922
VERSION
AE012522.1 GI:21115271
KEYWORDS
Xanthomonas campestris pv. campestris str. ATCC 33913.
SOURCE
Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
Xanthomonas.
REFERENCE
1 (bases 1 to 10895)
da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,
Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida
Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,
Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardoso,J.,
Chambergo,F., Clapina,L.P., Cicarelli,R.M.B., Coutinho,L.L.,
Curcio-Santos,J.R., El-Dorri,H., Faria,J.B., Ferreira,A.J.S.,
Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C.,
Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite
Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locati,E.C., Machado,M.A.,
Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J.,
Mench,C.F.N., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,
Okura,K.K., Oliveira,R.C., Oliveira,V.R., Pereira Jr.,H.A.,
Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F.,
Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos
Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and
Kitajima,J.P.
```



```

gene      5308. 6210
/ gene="rapk"
/ note="XCC4014"
CDS      5308. 6210
/ gene="rapk"
/ note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="pteridine-dependent deoxygenase like protein"
/protein_id="AAM3335.1"
/db_xref="GI:21115379"
/translacion="MLAVEGCGAARLDPRLVPLQVPAADVLVMTDAPVRG
RGNTAMSGRLOFCVIEIQEVEIEAAKAKAETATVSYSCOPFELIHWYLD
ATLGSDBREYVFCVAGSLGAVAGLNAVAGRCDAEITOTIWLAAADACT
PLENPROVSNYVPROGPOPSPARAMUPAGGDMPLLSGTAANGVASHHTQQLL
AQEETTFANFDELGAARHAFGLPAQFGAGTRLKYVVRERDLPKVALQADRFGDA
VRLHLUAYICRELAELVADGVHG"
complement(6270..7805)
/ gene="XCC4015"
complement(6270..7805)
/ gene="XCC4015"
/ note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="AMP-ligase"

Query Match      4.1%; Score 18; DB 1; Length 10895;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 CAGCGGGTGGTGGCGATG 105
|||||
Db 5012 CAGCGCGTGGTGGCGATG 5029

RESULT 9
AE011785
LOCUS      Xanthomonas axonopodis pv. citri str. 306, BCT 29-MAY-2002
DEFINITION the complete genome.
ACCESSION      AE011785 AE008923
VERSION      AE011785.1 GI:21107708
KEYWORDS
SOURCE      Xanthomonas axonopodis pv. citri str. 306.
Xanthomonas axonopodis pv. citri str. 306.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
Xanthomonas.
REFERENCE
1 (bases 1 to 11903)
da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,
Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida
Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,
Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,
Cursino-Santos,J.R., El-Dorri,H., Faria,J.B., Ferreira,A.J.S.,
Ferreira,R.C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite
Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,
Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meldanis,J.,
Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,
Okura,Y.K., Oliveira,M.C., Oliveira,V.R., Pereira,Jr.,H.A.,
Rosti,A., Sena,J.A.D., Silva,C. de Souza,R.F., Spicola,L.A.F.,
Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos
Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and
Kitajima,J.P.
Comparison of the genomes of two Xanthomonas pathogens with
differing host specificities
NATURE 417 (6887), 459-463 (2002)
MEDLINE      22022145
PUBMED      12024217
REFERENCE
2 (bases 1 to 11903)
da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,
Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida
Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,
Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,
Cursino-Santos,J.R., El-Dorri,H., Faria,J.B., Ferreira,A.J.S.,
Ferreira,R.C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite
Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,
Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meldanis,J.,
Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,
Okura,Y.K., Oliveira,M.C., Oliveira,V.R., Pereira,Jr.,H.A.,
Rosti,A., Sena,J.A.D., Silva,C. de Souza,R.F., Spicola,L.A.F.,
Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos
Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and
Kitajima,J.P.
Direct Submission
Submitted (28 Nov-2001) Departamento de Bioquímica, Universidade de
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
Brazil
FEATURES
source
Location/Qualifiers
1. 11903
/organism="Xanthomonas axonopodis pv. citri str. 306"
/strain="306"
/db_xref="taxon:190486"
/ note="pathovar: citri"
complement(151..1860)
/ gene="draA"
/ note="XAC1530"
complement(151..1860)
/ gene="draA"
/ note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="ABC transporter ATP-binding protein"
/protein_id="AAM36309.1"
/db_xref="GI:21107709"
/translacion="MPPFIQRGRGLFVAVVVALTISAATLSLPAVKRMIDQGFSGD
AQINQALFVSVVLAVATVAFYVALLGKVVADLRGLRHLNHLIDAGFHDRS
RGSVLRSLSAGLSLQSTMSVALSVATVIGSVVMLFVPSPLAGFTLIGPL
AVLPIVLGARLQIKISASODRVADANTLAAETLGAIVTQVHAREYRSQRFSTALL
TAIDAKVRIQTQVTAIVMLFGAIVLWGHADVIGRMTPTLQGFVLVALL
GGSGVLAELVWNLQAGMGVRSVSELDEQPLIVAPATQALPLRGALHFDQVY
FHYHPDPALPDFLHVSGTVALVPGSGAGKSTVLSMLRFHDPVSGKVRDDI
DURDADPVLLREHTALVPPQPTLFAASADNIRYGRHLNLLDEATSLADHSAERAVQQA
ALPQGYASEIGERGLSGGQQQVATARALLKADAPILLLLDEATSLADHSAERAVQQA
LERLMGEFTLVIAHRLATVLRKADRVVMDAGRIVAQGTHAQLTAEGGLYSLARLQF
IDO"
complement(1917..2510)
/ gene="XAC1531"
complement(1917..2510)
/ gene="XAC1531"
/ note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM36400.1"
/db_xref="GI:21107710"
/translacion="MLDTLADAHSLDIKHSPLARAAALETPAALLETIVORVAPED
ATHNWATRFQDYRSSDDGSGTAGCRPLANLQCGFDRVYVWYGGIKLGAG
GLVYAGTGAECRLATROPFLSLRSVQCRRDDQLGFLVHALPAFHADKLDERFDA
EGAAUVLPADQLAGLTKRCDATRNVRHLSTPEAA"
complement(2744..3337)
/ gene="XAC1532"
complement(2744..3337)
/ gene="XAC1532"
/ note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM36401.1"

```

```

/db_xref="GI:21107711"
/translation="NRSICVCGSNAGNKPAYVERATALGDRIAKOGRLVYGGNGV
LMGVANVLAAGGVTPIQOALADWEVHAHRLTLEIVGSMHERRMFLSDAFV
ADLPFGTMEIEPEIMWROITGNKPCAFDIEGYPALIGMDRMVEERFLHPDQR
ADLYGADIQMLEWQITPAQASKWIDEKRSTLV"
complement(3492..4928)
/gene="ldp"
/feature="ldp"
/note="XAC1533"
complement(3492..4928)
/gene="ldp"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="dihydrolipoamide dehydrogenase"
/protein_id="AAM36402.1"
/db_xref="GI:21107712"
/translation="MSEQFDVVVIGAGPAGYAAIRAAOIKMKVACIDRALCKGKPA
LGGTCLRVGIFSKALDSSQFQWNGHLPFGDHISFNDAKMDVPTNIGRKDKVQK
TGGALVFKANKITPYFGGQGNIVKYQHEGGEIEKLGNTVILAAAGESIELEFP
AKFGDRTIDVNGGLDFTAVPKRLAVIGAGVIGELGSLVYMKRGLAEVTILEALPDFLA
LADAERAKLFEKFGKGLDILKGAIVGKTEITGSDDAKQVLSYTDAGTGTVDK
LLVAVGAELKKNLADGTGVKVDGQIEVDGHCHTGVDGVAIGDCVYRGPMLAHKG
FEEGIAVAAELIAGLGHVFTDTPWYIYTEPEIAVWGKTEQQLKAEGVAYKAGSFPFA
ICHGRAVANGEPAGVKTADAEATDVLGMHLVGVGVSELVHEGLVTFEFGSADLLAR
ICHAAPTLSAIDHAAMAVSKRAIHKAN"
complement(5075..6286)
/gene="sucB"
/note="XAC1534"
complement(5075..6286)
/gene="sucB"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="dihydrolipoamide S-succinyltransferase"
/protein_id="AAM36403.1"
/db_xref="GI:21107713"
/translation="MATEVKVPVLPSVSDATIASHHKAGEAVKDENLVLETDKV
VLEPSPVGVKTEKFEQVTSNSGILAIIEGVAANAAPAFKORAAAPAAAP
AAAPGASGAARPEERPMVTRKTIAKLIMESKNSATMLTNEVNLAKVSAARKL
KAGGVKAGSARPEERPMVTRKTIAKLIMESKNSATMLTNEVNLAKVSAARKL
QDEPKAGKLGFGMSFVKAANAARLPVYNASIDGDLIYHGSYDSTIAVSTKGL
LVTPVNRVQSGFADVEQTDGTYAARAKAGKGLDLOGGTTITNGTFCGLSLTP
LIINPQSAIILGMHAIKRPPIAENGQVVIAPMYLALSVDHRIIDGKDSVQFLVDIKNQ
LENPQIMFGL"
complement(6329..9232)
/gene="odhA"
/note="XAC1535"
complement(6329..9232)
/gene="odhA"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="oxoglutarate dehydrogenase"
/protein_id="AAM36404.1"
/db_xref="GI:21107714"
/translation="MRPTDASRPAASAQSPQOFTRLIIVNLLKOFASOQLAGNNA
ATIEDVLEQVLVAPSDVPKWSYFDGFEGRGQDVPHSAIAHILAAKQANAGTG
AGSDERENRGLITAYKAGHQAQLDPLGLVPPVNPDDLPFHSUSQADIDSEF
STGVGQGPQRMKLDLLTRIKATYASIGAEPMHFOEPDQWYKRLSDAGKFIAGD
AASRRKTRLETLAEGRLYLRHYVQGRKFLSEGGDSLIIPMDDETIRQSSNDQVKOI
VIGMAHRCRLNVINTLGNPKRKLFEDEKFEHAHDHRRDGTGVYKHGFSADIAVIG
TKDVQVHALAFNPSHLEIVDVVWGVSVRSRQRFQDAPKRSVLPILIHGDAAFAQGV
VITMELPQSOARGFAGVGVTHIVVWNOIGFTTTRDDARSTLYCTDVARKMGAPFVHV
GDPPDAVNFVSKLAYEFQPKQDVLDVLCYRRMGHNEDEPAATQPVNYQTIKHKH
TTRLYAAKLESSEGLVSDAEKALVDYRNKLDGSEYTTTELAKRPDEFAIDMSYLV
GTAADVDVTRDQDLQDLAKLITTIPEGVELHARVAKIYEDRKVMAAGDQLGDWGA
ENLAVATLLAAGHKLRLVGDAAGRTGTFRHAILHDQTDIDYLPRLVLPVNPEDATV
DISLSLEAVMGVEYGVSTPDNALCLWEAOFDGAQGVVDOFTAAEAKWGRITA
GLSLFLPHGVGEGGPHSSRFLPQICALENLVVCYPTTPAQCEHMRORMTTR
KFLVMTTPKSLRKLAVSSLEELADGQFQHLIPDAKAAKVRHVVLCGSKVYDILL

```

```

EDQTKRGQDQVALLRVEQLYFPRAQLAAELKAYANATDVVWCQEPQNOGANTQIRH
HUNFLAGGQSLHYAGRAKSPSPAAGHMADHIIEOCKULVADALLNPFNOVAE"
complement(9338..10267)
/gene="XAC1536"
complement(9338..10267)
/gene="XAC1536"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM36405.1"
/db_xref="GI:21107715"
/translation="MTAHARPOIVTLDPRADAALRALRLACATDTAGATGQVMDAL
DPLSLHVAEAGOLIASVELTADRRDLGLVSNRRSGVADQLLAAYDAARQSGM
PGLRACSPAAEAVFARLGLPDAETLSSPERIGOTHDAGCTVYHRLGQPMVDSGT
ALAAATGLCAARQVLYITRALDPAFNAVLDALREATARHDKRVHVLVODTA
SAAASSAMULRAQRLPVSFRFRVADPDAFSFVYVGGDDIAYFRPTGHRFDDGRT
WUSGAARSQRLEREPACIWIERSALWNEPRAIGI"
complement(10264..11751)
Query Match 4.1%; Score 18; DB 1; Length 11903;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 71 CCGCGCGGCGAGCGAGGCG 88
Db 6414 CCGCGCGGCGAGCGAGGCG 6431

RESULT 10
AC014124 36690 bp DNA linear HTG 16-NOV-1999
LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***
DEFINITION AC014124.1 GI:6437211
VERSION AC014124.1 GI:6437211
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Drosophila melanogaster.
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 36690)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10213424 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source Location/Qualifiers
1..36690
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 10595 a 7518 c 7672 g 10905 t
ORIGIN
Query Match 4.1%; Score 18; DB 2; Length 36690;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 68 TCACCGCGCGAGCGAG 85
Db 27867 TCACCGCGCGAGCGAG 27884

RESULT 11
AC062001 82815 bp DNA linear HTG 21-APR-2000
LOCUS

```

```

DEFINITION Homo sapiens Chromosome 4 clone RP11-124H2 map 4, LOW-PASS SEQUENCE
ACCESSION AC062001
VERSION AC062001.1 GI:7630740
KEYWORDS HTG; HTGS-PHASE0.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
1 (bases 1 to 82815)
2 (bases 1 to 82815)
AUTHORS Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
Boguslavsky, L., Bouckhalder, B., Brown, A., Burkett, G.,
Campoliano, A., Castile, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Melidrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Ollivar, T.M., Oliver, J., Peterson, K., Pliere, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stefanovic, N., Subramanian, A., Talanas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Triggilio, J.,
Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (21-Apr-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: I9871
Center clone name: 124_H2
-----
* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 976 1075: gap of 100 bp
* 1076 2100: contig of 1025 bp in length
* 2101 2200: gap of 100 bp
* 2201 3185: contig of 985 bp in length
* 3186 3285: gap of 100 bp
* 3286 4151: contig of 866 bp in length
* 4152 4251: gap of 100 bp
* 4252 5206: contig of 955 bp in length
* 5207 5306: gap of 100 bp
* 5307 6287: contig of 961 bp in length
* 6288 6387: gap of 100 bp
*
* 6388 7332: contig of 945 bp in length
* 7333 7432: gap of 100 bp
* 7433 8397: contig of 965 bp in length
* 8398 8497: gap of 100 bp
* 8498 9457: contig of 960 bp in length
* 9458 9557: gap of 100 bp
* 9558 10489: contig of 932 bp in length
* 10490 10589: gap of 100 bp
* 10590 11602: contig of 1013 bp in length
* 11603 11702: gap of 100 bp
* 11703 12694: contig of 992 bp in length
* 12695 13798: contig of 1004 bp in length
* 13799 13898: gap of 100 bp
* 13899 14866: contig of 968 bp in length
* 14867 14966: gap of 100 bp
* 14967 15930: contig of 964 bp in length
* 15931 16030: gap of 100 bp
* 16031 16981: contig of 951 bp in length
* 16982 17081: gap of 100 bp
* 17082 18043: contig of 962 bp in length
* 18044 18143: gap of 100 bp
* 18144 19119: contig of 976 bp in length
* 19120 19219: gap of 100 bp
* 19220 20173: contig of 954 bp in length
* 20174 20273: gap of 100 bp
* 20274 21232: contig of 959 bp in length
* 21233 21332: gap of 100 bp
* 21333 22227: contig of 895 bp in length
* 22228 22327: gap of 100 bp
* 22329 23303: contig of 976 bp in length
* 23304 23403: gap of 100 bp
* 23404 24393: contig of 990 bp in length
* 24394 24493: gap of 100 bp
* 24494 25495: contig of 1002 bp in length
* 25496 25595: gap of 100 bp
* 25596 26554: contig of 959 bp in length
* 26555 26654: gap of 100 bp
* 26655 27611: contig of 957 bp in length
* 27612 27711: gap of 100 bp
* 27712 28689: contig of 978 bp in length
* 28690 28789: gap of 100 bp
* 28790 29750: contig of 961 bp in length
* 29751 29850: gap of 100 bp
* 29851 30790: contig of 940 bp in length
* 30791 30890: gap of 100 bp
* 30891 31881: contig of 991 bp in length
* 31882 31981: gap of 100 bp
* 31982 32962: contig of 981 bp in length
* 32963 33062: gap of 100 bp
* 33063 34046: contig of 984 bp in length
* 34047 34146: gap of 100 bp
* 34147 35108: contig of 962 bp in length
* 35109 35208: gap of 100 bp
* 35209 36136: contig of 928 bp in length
* 36137 36236: gap of 100 bp
* 36237 37202: contig of 966 bp in length
* 37203 37302: gap of 100 bp
* 37303 38272: contig of 970 bp in length
* 38273 38372: gap of 100 bp
* 38373 39319: contig of 947 bp in length
* 39320 39419: gap of 100 bp
* 39420 40376: contig of 957 bp in length
* 40377 40476: gap of 100 bp
* 40477 41464: contig of 988 bp in length
* 41465 41564: gap of 100 bp
* 41565 42492: contig of 928 bp in length
* 42493 42592: gap of 100 bp
* 42593 43578: contig of 986 bp in length
* 43579 43678: gap of 100 bp
* 43679 44686: contig of 1008 bp in length
* 44687 44786: gap of 100 bp
* 44787 45745: contig of 959 bp in length

```

\* 45746 45845: gap of 100 bp  
 \* 45846 45827: contig of 982 bp in length  
 \* 46828 46927: gap of 100 bp  
 \* 47911 48010: contig of 983 bp in length  
 \* 48011 48969: contig of 959 bp in length  
 \* 48970 49069: gap of 100 bp  
 \* 49070 50028: contig of 959 bp in length  
 \* 50029 50128: gap of 100 bp  
 \* 50129 51053: contig of 925 bp in length  
 \* 51054 51153: gap of 100 bp  
 \* 51154 52111: contig of 958 bp in length  
 \* 52112 52211: gap of 100 bp  
 \* 52212 53189: contig of 978 bp in length  
 \* 53190 53289: gap of 100 bp  
 \* 53290 54271: contig of 982 bp in length  
 \* 54272 54371: gap of 100 bp  
 \* 54372 55336: contig of 965 bp in length  
 \* 55337 55436: gap of 100 bp  
 \* 55437 56366: contig of 930 bp in length  
 \* 56367 56466: gap of 100 bp  
 \* 56467 57415: contig of 949 bp in length  
 \* 57416 57515: gap of 100 bp  
 \* 57516 58501: contig of 986 bp in length  
 \* 58502 58601: gap of 100 bp  
 \* 58602 59567: contig of 966 bp in length  
 \* 59568 59667: gap of 100 bp  
 \* 59668 60585: contig of 918 bp in length  
 \* 60586 60685: gap of 100 bp  
 \* 60686 61646: contig of 961 bp in length  
 \* 61647 61746: gap of 100 bp  
 \* 61747 62739: contig of 953 bp in length  
 \* 62740 62839: gap of 100 bp  
 \* 62840 63824: contig of 985 bp in length  
 \* 63825 63924: gap of 100 bp  
 \* 63925 64903: contig of 979 bp in length  
 \* 64904 65003: gap of 100 bp  
 \* 65004 65366: contig of 960 bp in length  
 \* 65367 66663: gap of 100 bp  
 \* 66664 67010: contig of 947 bp in length  
 \* 67011 67110: gap of 100 bp  
 \* 67111 68077: contig of 967 bp in length  
 \* 68078 68177: gap of 100 bp  
 \* 68178 69147: contig of 970 bp in length  
 \* 69148 69247: gap of 100 bp  
 \* 69248 70258: contig of 1011 bp in length  
 \* 70259 70358: gap of 100 bp  
 \* 70359 71286: contig of 928 bp in length  
 \* 71287 71386: gap of 100 bp  
 \* 71387 72279: contig of 893 bp in length  
 \* 72280 72379: gap of 100 bp  
 \* 72380 73317: contig of 938 bp in length  
 \* 73318 73417: gap of 100 bp

Query Match 4.1%; Score 18; DB 2; Length 82815;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTTTTCGTCGCCGCGTC 39  
 DB 78533 CTTTTCGTCGCCGCGTC 78550  
 |||||

RESULT 12  
 LOCUS RCU57682 86896 bp DNA linear BCT 07-FEB-1997  
 DEFINITION Rhodobacter capsulatus cosmids 143-147, complete sequence.  
 ACCESSION U57682  
 VERSION U57682.1 GI:1613791  
 KEYWORDS HTG  
 SOURCE Rhodobacter capsulatus  
 ORGANISM Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;

REFERENCE  
 AUTHORS Kumar,V., Fonstein,M. and Haselkorn,R.  
 JOURNAL Bacterium genome sequence  
 MEDLINE Nature 381 (6584), 653-654 (1996)  
 PUBMED 9680014  
 8649508  
 REFERENCE  
 AUTHORS Fonstein,M., Kumar,V. and Haselkorn,R.  
 JOURNAL Direct Submission  
 TITLE Submitted (07-MAY-1996) M. Fonstein, MGSB, Univ of Chicago, 920 E.  
 JOURNAL 58th, Chicago, IL 60637, USA  
 FEATURES  
 source  
 Location/Qualifiers  
 1..86896  
 /organism="Rhodobacter capsulatus"  
 /strain="861003"  
 /db\_xref="taxon:1061"  
 /map="cosmids 143-147 of the complete encyclopedia"  
 1 others

BASE COUNT 15089 a 28056 c 28787 g 14963 t  
 ORIGIN  
 Query Match 4.1%; Score 18; DB 1; Length 86896;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 AGCGTGGCGTCACGCGC 75  
 |||||

DB 76328 AGCGTGGCGTCACGCGC 76311  
 |||||

RESULT 13  
 LOCUS AP003026/c 104802 bp DNA linear PRI 18-JUL-2001  
 DEFINITION Homo sapiens genomic DNA, chromosome 11q, clone:RP11-21N9, complete  
 sequence.  
 ACCESSION AP003026  
 VERSION AP003026.2 GI:14861119  
 KEYWORDS HTG.  
 SOURCE Homo sapiens DNA, clone:RP11-21N9.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 TITLE Published Only in Database (2000)

REFERENCE  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 JOURNAL Direct Submission  
 TITLE Submitted (08-DEC-2000) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:hattori@gs.c.riken.go.jp, URL:http://hgp-gsc.riken.go.jp/,  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 COMMENT On Jul 17, 2001 this sequence version replaced gi:11611633.  
 FEATURES  
 source  
 Location/Qualifiers  
 1..104802  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="11"  
 /map="11q"  
 /clone="RP11-21N9"

BASE COUNT 32096 a 20123 c 20154 g 32429 t  
 ORIGIN

Query Match 4.1%; Score 18; DB 9; Length 104802;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 TATACCATTTTGTCAACC 253  
 |||||

Db 31508 TATACCATTTTGTCAAGC 31491

RESULT 14  
LMFLCHR31\_13

WPCOMMENT

Sequence split into 22 fragments LOCUS LMFLCHR31 Accession AL499621

Fragment Name	Begin	End
LMFLCHR31_00	1	110000
LMFLCHR31_01	100001	210000
LMFLCHR31_02	200001	310000
LMFLCHR31_03	300001	410000
LMFLCHR31_04	400001	510000
LMFLCHR31_05	500001	610000
LMFLCHR31_06	600001	710000
LMFLCHR31_07	700001	810000
LMFLCHR31_08	800001	910000
LMFLCHR31_09	900001	1010000
LMFLCHR31_10	1000001	1110000
LMFLCHR31_11	1100001	1210000
LMFLCHR31_12	1200001	1310000
LMFLCHR31_13	1300001	1410000
LMFLCHR31_14	1400001	1510000
LMFLCHR31_15	1500001	1610000
LMFLCHR31_16	1600001	1710000
LMFLCHR31_17	1700001	1810000
LMFLCHR31_18	1800001	1910000
LMFLCHR31_19	1900001	2010000
LMFLCHR31_20	2000001	2110000
LMFLCHR31_21	2100001	2117963

Db 19748 GCGGTGGTGGCGATGGCG 19765

Search completed: November 30, 2002, 03:35:24  
Job time : 3259 secsLMFLCHR32\_27 2700001 2727709  
Continuation (22 of 28) of LMFLCHR32 from base 2100001 (AL499622 Leishmania major chr

Query Match 4.1%; Score 18; DB 2: Length 110000;

Best Local Similarity 100.0%; Pred. No. 80;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 GCGGTGGTGGCGATGGCG 108

|||||

Db 19748 GCGGTGGTGGCGATGGCG 19765

Continuation (14 of 22) of LMFLCHR31 from base 1300001 (AL499621 Leishmania major chromo

Query Match 4.1%; Score 18; DB 2: Length 110000;

Best Local Similarity 100.0%; Pred. No. 80;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 GCGGTGGTGGCGATGGCG 108

|||||

Db 38174 GCGGTGGTGGCGATGGCG 38191

RESULT 15  
LMFLCHR32\_21

WPCOMMENT

Sequence split into 28 fragments LOCUS LMFLCHR32 Accession AL499622

Fragment Name	Begin	End
LMFLCHR32_00	1	110000
LMFLCHR32_01	100001	210000
LMFLCHR32_02	200001	310000
LMFLCHR32_03	300001	410000
LMFLCHR32_04	400001	510000
LMFLCHR32_05	500001	610000
LMFLCHR32_06	600001	710000
LMFLCHR32_07	700001	810000
LMFLCHR32_08	800001	910000
LMFLCHR32_09	900001	1010000
LMFLCHR32_10	1000001	1110000
LMFLCHR32_11	1100001	1210000
LMFLCHR32_12	1200001	1310000
LMFLCHR32_13	1300001	1410000
LMFLCHR32_14	1400001	1510000
LMFLCHR32_15	1500001	1610000
LMFLCHR32_16	1600001	1710000
LMFLCHR32_17	1700001	1810000
LMFLCHR32_18	1800001	1910000
LMFLCHR32_19	1900001	2010000
LMFLCHR32_20	2000001	2110000
LMFLCHR32_21	2100001	2210000
LMFLCHR32_22	2200001	2310000
LMFLCHR32_23	2300001	2410000
LMFLCHR32_24	2400001	2510000
LMFLCHR32_25	2500001	2610000
LMFLCHR32_26	2600001	2710000





PR	19-APR-1999;	99US-0130077;	PR	19-JUL-1999;	99US-0144335;
PR	21-APR-1999;	99US-0130449;	PR	20-JUL-1999;	99US-0144352;
PR	23-APR-1999;	99US-0130510;	PR	20-JUL-1999;	99US-0144632;
PR	25-APR-1999;	99US-0130801;	PR	20-JUL-1999;	99US-0144884;
PR	28-APR-1999;	99US-0131449;	PR	21-JUL-1999;	99US-0144814;
PR	30-APR-1999;	99US-0132046;	PR	21-JUL-1999;	99US-0145086;
PR	04-MAY-1999;	99US-0132407;	PR	21-JUL-1999;	99US-0145088;
PR	05-MAY-1999;	99US-0132484;	PR	22-JUL-1999;	99US-0145085;
PR	06-MAY-1999;	99US-0132485;	PR	22-JUL-1999;	99US-0145087;
PR	06-MAY-1999;	99US-0132486;	PR	22-JUL-1999;	99US-0145089;
PR	07-MAY-1999;	99US-0132487;	PR	22-JUL-1999;	99US-0145192;
PR	07-MAY-1999;	99US-0132863;	PR	23-JUL-1999;	99US-0145145;
PR	11-MAY-1999;	99US-0134256;	PR	23-JUL-1999;	99US-0145218;
PR	14-MAY-1999;	99US-0134218;	PR	23-JUL-1999;	99US-0145224;
PR	14-MAY-1999;	99US-0134219;	PR	26-JUL-1999;	99US-0145276;
PR	14-MAY-1999;	99US-0134221;	PR	27-JUL-1999;	99US-0145913;
PR	14-MAY-1999;	99US-0134370;	PR	27-JUL-1999;	99US-0145918;
PR	18-MAY-1999;	99US-0134768;	PR	27-JUL-1999;	99US-0145919;
PR	19-MAY-1999;	99US-0134941;	PR	28-JUL-1999;	99US-0145951;
PR	20-MAY-1999;	99US-0135124;	PR	02-AUG-1999;	99US-0146386;
PR	21-MAY-1999;	99US-0135353;	PR	02-AUG-1999;	99US-0146388;
PR	24-MAY-1999;	99US-0135629;	PR	02-AUG-1999;	99US-0146389;
PR	25-MAY-1999;	99US-0136021;	PR	03-AUG-1999;	99US-0147038;
PR	27-MAY-1999;	99US-0136392;	PR	04-AUG-1999;	99US-0147204;
PR	28-MAY-1999;	99US-0136782;	PR	05-AUG-1999;	99US-0147302;
PR	01-JUN-1999;	99US-0137222;	PR	05-AUG-1999;	99US-0147192;
PR	03-JUN-1999;	99US-0137528;	PR	05-AUG-1999;	99US-0147260;
PR	04-JUN-1999;	99US-0137502;	PR	06-AUG-1999;	99US-0147303;
PR	07-JUN-1999;	99US-0137724;	PR	06-AUG-1999;	99US-0147416;
PR	08-JUN-1999;	99US-0138094;	PR	09-AUG-1999;	99US-0147493;
PR	10-JUN-1999;	99US-0138540;	PR	09-AUG-1999;	99US-0147935;
PR	14-JUN-1999;	99US-0138847;	PR	09-AUG-1999;	99US-0148171;
PR	14-JUN-1999;	99US-0139119;	PR	11-AUG-1999;	99US-0148119;
PR	16-JUN-1999;	99US-0139432;	PR	12-AUG-1999;	99US-0148241;
PR	16-JUN-1999;	99US-0139453;	PR	13-AUG-1999;	99US-0148565;
PR	17-JUN-1999;	99US-0139492;	PR	13-AUG-1999;	99US-0148684;
PR	18-JUN-1999;	99US-0139494;	PR	16-AUG-1999;	99US-0149368;
PR	18-JUN-1999;	99US-0139455;	PR	17-AUG-1999;	99US-0149175;
PR	18-JUN-1999;	99US-0139456;	PR	18-AUG-1999;	99US-0149426;
PR	18-JUN-1999;	99US-0139457;	PR	20-AUG-1999;	99US-0149722;
PR	18-JUN-1999;	99US-0139458;	PR	20-AUG-1999;	99US-0149723;
PR	18-JUN-1999;	99US-0139459;	PR	20-AUG-1999;	99US-0149929;
PR	18-JUN-1999;	99US-0139460;	PR	23-AUG-1999;	99US-0149902;
PR	18-JUN-1999;	99US-0139461;	PR	23-AUG-1999;	99US-0149930;
PR	18-JUN-1999;	99US-0139462;	PR	25-AUG-1999;	99US-0150566;
PR	18-JUN-1999;	99US-0139463;	PR	26-AUG-1999;	99US-0150884;
PR	18-JUN-1999;	99US-0139750;	PR	27-AUG-1999;	99US-0151065;
PR	18-JUN-1999;	99US-0139763;	PR	27-AUG-1999;	99US-0151066;
PR	21-JUN-1999;	99US-0139817;	PR	27-AUG-1999;	99US-0151080;
PR	22-JUN-1999;	99US-0139899;	PR	30-AUG-1999;	99US-0151303;
PR	23-JUN-1999;	99US-0140353;	PR	31-AUG-1999;	99US-0151438;
PR	23-JUN-1999;	99US-0140354;	PR	01-SEP-1999;	99US-0151930;
PR	24-JUN-1999;	99US-0140695;	PR	07-SEP-1999;	99US-0152363;
PR	25-JUN-1999;	99US-0140823;	PR	10-SEP-1999;	99US-0153070;
PR	25-JUN-1999;	99US-0140991;	PR	13-SEP-1999;	99US-0153758;
PR	30-JUN-1999;	99US-0141287;	PR	15-SEP-1999;	99US-0154018;
PR	01-JUL-1999;	99US-0141842;	PR	16-SEP-1999;	99US-0154039;
PR	01-JUL-1999;	99US-0142154;	PR	20-SEP-1999;	99US-0154779;
PR	02-JUL-1999;	99US-0142055;	PR	23-SEP-1999;	99US-0155139;
PR	08-JUL-1999;	99US-0142390;	PR	23-SEP-1999;	99US-01553486;
PR	08-JUL-1999;	99US-0142803;	PR	28-SEP-1999;	99US-0155659;
PR	09-JUL-1999;	99US-0142920;	PR	29-SEP-1999;	99US-0156458;
PR	12-JUL-1999;	99US-0142977;	PR	29-SEP-1999;	99US-0156596;
PR	13-JUL-1999;	99US-0143542;	PR	04-OCT-1999;	99US-0157117;
PR	14-JUL-1999;	99US-0143624;	PR	05-OCT-1999;	99US-0157753;
PR	15-JUL-1999;	99US-0144005;	PR	06-OCT-1999;	99US-0157865;
PR	16-JUL-1999;	99US-0144085;	PR	07-OCT-1999;	99US-0158029;
PR	16-JUL-1999;	99US-0144086;	PR	08-OCT-1999;	99US-0158232;
PR	19-JUL-1999;	99US-0144325;	PR	12-OCT-1999;	99US-0158369;
PR	19-JUL-1999;	99US-0144331;	PR	13-OCT-1999;	99US-0159293;
PR	19-JUL-1999;	99US-0144332;	PR	13-OCT-1999;	99US-0159294;
PR	19-JUL-1999;	99US-0144333;	PR	13-OCT-1999;	99US-0159295;
PR	19-JUL-1999;	99US-0144334;	PR	14-OCT-1999;	99US-0159329;

```

PR 14-OCT-1999; 99US-0159130.
PR 14-OCT-1999; 99US-0159131.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159638.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 7.7%; Score 34; DB 21; Length 462;
Best Local Similarity 100.0%; Prid. No. 1.1e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 53
    |||||
Db 61 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 94

RESULT 2
ARC43563
XX AAC43563 standard; DNA; 405 BP.
XX AAC43563;
XX 17-OCT-2000 (first entry)
XX Zea mays DNA fragment SEQ ID NO: 39686.
XX Zea mays DNA fragment SEQ ID NO: 39686.
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic;
XX pathway; promoter; termination sequence; corn; ss.
XX Zea mays subsp. mays.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123348.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129645.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130810.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134221.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
XX 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
XX 16-JUN-1999; 99US-0139452.
XX 16-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.
XX 18-JUN-1999; 99US-0139454.
XX 18-JUN-1999; 99US-0139455.
XX 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
XX 18-JUN-1999; 99US-0139458.
XX 18-JUN-1999; 99US-0139459.
XX 18-JUN-1999; 99US-0139460.
XX 18-JUN-1999; 99US-0139461.
XX 18-JUN-1999; 99US-0139462.
XX 18-JUN-1999; 99US-0139463.
XX 18-JUN-1999; 99US-0139750.
XX 18-JUN-1999; 99US-0139763.
XX 21-JUN-1999; 99US-0139817.
XX 22-JUN-1999; 99US-0139899.
XX 23-JUN-1999; 99US-0140353.
XX 23-JUN-1999; 99US-0140354.
XX 24-JUN-1999; 99US-0140695.
XX 28-JUN-1999; 99US-0140823.
XX 29-JUN-1999; 99US-0140991.
XX 30-JUN-1999; 99US-0141287.
XX 01-JUL-1999; 99US-014154.
XX 01-JUL-1999; 99US-014154.
XX 02-JUL-1999; 99US-0142055.
XX 06-JUL-1999; 99US-0142390.
XX 08-JUL-1999; 99US-0142803.
XX 09-JUL-1999; 99US-0142920.
XX 12-JUL-1999; 99US-0142977.
XX 13-JUL-1999; 99US-0143542.
XX 14-JUL-1999; 99US-0143624.
XX 15-JUL-1999; 99US-0144005.
XX 16-JUL-1999; 99US-0144085.
XX 16-JUL-1999; 99US-0144086.
XX 19-JUL-1999; 99US-0144325.
XX 19-JUL-1999; 99US-0144331.
XX 19-JUL-1999; 99US-0144332.
XX 19-JUL-1999; 99US-0144333.
XX 19-JUL-1999; 99US-0144334.
XX 19-JUL-1999; 99US-0144335.
XX 20-JUL-1999; 99US-0144352.
XX 20-JUL-1999; 99US-0144632.
XX 20-JUL-1999; 99US-0144684.
XX 21-JUL-1999; 99US-0144814.
XX 21-JUL-1999; 99US-0145086.
XX 21-JUL-1999; 99US-0145088.

```

```
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145091.
PR 22-JUL-1999; 99US-0145152.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 23-JUL-1999; 99US-0145276.
PR 26-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 27-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0145986.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148694.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149368.
PR 18-AUG-1999; 99US-0149446.
PR 18-AUG-1999; 99US-0149446.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 08-OCT-1999; 99US-0157753.
PR 08-OCT-1999; 99US-0157855.
PR 07-OCT-1999; 99US-0158025.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.

PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 5.9%; Score 26; DB 21; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 AGGCGAGCGGTGGTGGCGATGGCGT 109
|||||
Db 106 AGGCGAGCGGTGGTGGCGATGGCGT 131

RESULT 3
AAC51740
ID AAC51740 standard; DNA; 455 BP.
AC AAC51740;
XX
XX 18-OCT-2000 (first entry)
DE
DE zea mays DNA fragment SEQ ID NO: 69614.
KW Hybridization assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
OS zea mays subsp. mays.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 08-APR-1999; 99US-0128234.
XX 16-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0128845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 23-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
```

PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0143055.  
PR 08-JUL-1999; 99US-0143280.  
PR 09-JUL-1999; 99US-0142803.  
PR 12-JUL-1999; 99US-0142920.  
PR 13-JUL-1999; 99US-0142977.  
PR 14-JUL-1999; 99US-0143542.  
PR 15-JUL-1999; 99US-0143624.  
PR 16-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149902.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150886.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151086.  
PR 30-AUG-1999; 99US-0151193.  
PR 31-AUG-1999; 99US-0151436.  
PR 01-SEP-1999; 99US-0151520.  
PR 07-SEP-1999; 99US-0152263.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 13-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.

PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 4.5%; Score 20; DB 21; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 0.58; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0;

OY 20 CGCGTTTCGTCGCCGCGTC 39  
 |||||  
 DB 84 CGCGTTTCGTCGCCGCGTC 103  
 |||||

RESULT 4  
 AAZ52325  
 ID AAZ52325 standard; DNA; 1503 BP.  
 XX  
 AC AAZ52325;  
 XX  
 DT 24-JUL-2000 (first entry)  
 XX  
 DE Klebsiella oxytoca LyxK gene.  
 XX  
 KW LyxK-S operon; LyxK; YiaJ; regulatory sequence; YiaK; YiaL; ORF1; YiaX2;  
 KW YiaQ; YiaR; YiaS; carbohydrate utilisation; screening; metabolic pathway;  
 KW biological synthesis; anti-infective; antibacterial; ds.  
 XX  
 OS Klebsiella oxytoca.  
 XX  
 PW Key Location/Qualifiers  
 XX 1..1503  
 FT /tag- a  
 FT /product- "Klebsiella oxytoca LyxK protein"  
 FT /note- "Does not include stop codon"  
 FT /partial  
 XX  
 PW WO200022170-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 12-OCT-1999; 99WO-US23862.  
 XX  
 PR 14-OCT-1998; 98US-0172952.  
 XX  
 PA (MICR-) MICROGENOMICS INC.  
 XX  
 PI Hoch J, Dartois V;  
 XX  
 DR WPI; 2000-318013/27.  
 DR P-PSDB; AAY70727.  
 XX  
 PT Screening for metabolic pathways, useful to provide for the biological  
 PT production of chemicals, antibacterials and other anti-infectives,  
 PT using cells which provide a signal in the presence of a compound  
 PT produced by the pathway  
 XX  
 PS Claim 40a; Page 98-99; 137pp; English.  
 XX  
 CC The present DNA sequence is the Klebsiella oxytoca LyxK gene, of the  
 CC YiaK-S operon. It includes the genes encoding the Yia operon-related  
 CC polypeptides, YiaK, YiaL, ORF1, YiaX2, YiaQ, YiaR and YiaS. It is  
 CC preceded by the transcriptional regulatory sequence YiaJ. The function  
 CC of the Yia operon gene products are unknown. It is homologous to YiaK-S  
 CC operon of Escherichia coli and Haemophilus influenzae, which may be  
 CC involved in carbohydrate utilisation. The E.coli LyxK encoded enzyme  
 CC phosphorylates L-xylulose and plays an important role in the utilisation

CC of L-xylulose by E.coli. This operon is used in a method for screening  
 CC nucleotide sequences, the products of which can convert a source compound  
 CC to a target compound, using cells which can provide a detectable signal  
 CC in the presence of the target compound. This sequence is used to screen  
 CC and identify biological pathways, that can be used for the biological  
 CC synthesis of chemicals, antibacterials and other anti-infectives.  
 XX  
 SQ Sequence 1503 BP; 287 A; 463 C; 456 G; 297 T; 0 other;  
 Query Match 3.9%; Score 17; DB 21; Length 1503;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 TCGCGTCAACGCGCGC 78  
 |||||  
 DB 1199 TCGCGTCAACGCGCGC 1215  
 |||||

RESULT 5  
 ABL18169/c  
 ID ABL18169 standard; DNA; 2219 BP.  
 XX  
 AC ABL18169;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5980.  
 XX  
 KW Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ds.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PW WO200171042-A2.  
 XX  
 DT 27-SEP-2001.  
 XX  
 DT 23-MAR-2001; 2001WO-US09231.  
 XX  
 XX 23-MAR-2000; 2000US-1916376.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1; SEQ ID NO 5980; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 2219 BP; 523 A; 673 C; 579 G; 444 T; 0 other;  
 Query Match 3.9%; Score 17; DB 23; Length 2219;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 CGGTGGTGGCGATGGCG 108

Db 801 CGGTGGTGGCGATGGCG 785  
 |||||  
 RESULT 6  
 ABL14523/C  
 ID ABL14523 standard; CDNA; 2487 BP.  
 XX AC ABL14523;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38051.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical; gene; ss.  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US09231.  
 XX PR 23-MAR-2000; 2000US-191637P.  
 XX PR 11-JUL-2000; 2000US-0614150.  
 XX PA (PEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX PPI; 2001-656860/75.  
 XX DR P-PSDB; ABB70420.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.  
 XX PS Claim 1; SEQ ID NO 38051; 21bp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB116175-AB130511), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (AB57737-AB572072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 2487 BP; 608 A; 737 C; 639 G; 503 T; 0 other;  
 Query Match 3.9%; Score 17; DB 23; Length 2487;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 92 CGGTGGTGGCGATGGCG 108  
 |||||  
 Db 1069 CGGTGGTGGCGATGGCG 1053  
 RESULT 7  
 AAH67505  
 ID AAH67505 standard; DNA; 2844 BP.  
 XX AC AAH67505;  
 XX DT 26-SEP-2001 (first entry)  
 XX DE C glutamicum coding sequence fragment SEQ ID NO: 2540.  
 121  
 XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
 XX KW organic acid synthesis; ds.  
 XX OS Corynebacterium glutamicum.  
 XX PN EP1108790-A2.  
 XX PD 20-JUN-2001.  
 XX PF 18-DEC-2000; 2000EP-0127688.  
 XX PR 16-DEC-1999; 99JP-0377484.  
 XX PR 07-APR-2000; 2000JP-0159162.  
 XX PR 03-AUG-2000; 2000JP-0280988.  
 XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
 XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
 XX WPI; 2001-376931/40.  
 XX DR P-PSDB; AAG92286.  
 XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying  
 PT mutation point of a gene, measuring expression of a gene, analysing  
 PT expression profile or pattern of a gene and identifying homologous gene  
 PT  
 XX PS Claim 8; SEQ ID NO: 2540; 246pp + Sequence Listing; English.  
 XX CC The present invention provides a number of nucleotide and protein  
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
 CC are useful for identifying the mutation point of a gene derived from a  
 CC mutant of Coryneform bacterium, measuring expression amount and  
 CC analysing the expression profile or expression pattern of a gene derived  
 CC from Coryneform bacterium, and identifying a homologue of a gene derived  
 CC from Coryneform bacterium. Coryneform bacteria are useful for producing  
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
 CC particularly L-lysine. The present sequence is a nucleic acid described  
 CC in the exemplification of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC European Patent Office.  
 XX SQ Sequence 2844 BP; 676 A; 786 C; 760 G; 622 T; 0 other;  
 Query Match 3.9%; Score 17; DB 22; Length 2844;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CGCGCGCGACTTGGCC 23  
 |||||  
 Db 1896 CGCGCGCGACTTGGCC 1912  
 RESULT 8  
 AAF71426  
 ID AAF71426 standard; DNA; 2859 BP.  
 XX AC AAF71426;  
 XX DT 30-APR-2001 (first entry)  
 XX DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:133.  
 XX KW Corynebacterium glutamicum; carbon metabolism and energy production;  
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;  
 KW fine chemical production; organic acid; proteinogenic amino acid;  
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.

XX Corynebacterium glutamicum.  
 XX WO200100844-A2.  
 XX PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-IB00943.  
 XX PR 25-JUN-1999; 99US-0141031.  
 XX PR 08-JUL-1999; 99DE-1031412.  
 XX PR 08-JUL-1999; 99DE-1031413.  
 XX PR 08-JUL-1999; 99DE-1031419.  
 XX PR 08-JUL-1999; 99DE-1031420.  
 XX PR 08-JUL-1999; 99DE-1031424.  
 XX PR 08-JUL-1999; 99DE-1031426.  
 XX PR 08-JUL-1999; 99DE-1031431.  
 XX PR 08-JUL-1999; 99DE-1031433.  
 XX PR 08-JUL-1999; 99DE-1031434.  
 XX PR 08-JUL-1999; 99DE-1031510.  
 XX PR 08-JUL-1999; 99DE-1031562.  
 XX PR 08-JUL-1999; 99DE-1031634.  
 XX PR 08-JUL-1999; 99DE-1032180.  
 XX PR 08-JUL-1999; 99DE-1032247.  
 XX PR 08-JUL-1999; 99DE-1032250.  
 XX PR 08-JUL-1999; 99DE-0143208.  
 XX PR 14-JUL-1999; 99DE-1032934.  
 XX PR 14-JUL-1999; 99DE-1032973.  
 XX PR 14-JUL-1999; 99DE-1033005.  
 XX PR 27-AUG-1999; 99DE-1040755.  
 XX PR 31-AUG-1999; 99US-0151572.  
 XX PR 03-SEP-1999; 99DE-1042076.  
 XX PR 03-SEP-1999; 99DE-1042086.  
 XX PR 03-SEP-1999; 99DE-1042087.  
 XX PR 03-SEP-1999; 99DE-1042088.  
 XX PR 03-SEP-1999; 99DE-1042095.  
 XX PR 03-SEP-1999; 99DE-1042123.  
 XX PR 03-SEP-1999; 99DE-1042125.  
 XX PA (BADI ) BASF AG.  
 XX PI Pompejus M. Kroeger B, Schroeder H, Zeider O, Haberhauer G;  
 XX WPI; 2001-061975/07.  
 XX P-PSDB; AAB79309.  
 XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar  
 PT metabolism and oxidative phosphorylation protein for production or  
 PT modulation of production of fine chemicals e.g. amino acids,  
 PT carbohydrates or enzymes -  
 XX Claim 3; Page 342-345; 1246pp; English.  
 XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar  
 CC metabolism and oxidative phosphorylation (SMP) proteins given in  
 CC AAB79243 to AAB 79633 which are involved in carbon metabolism and  
 CC energy production. The C. glutamicum SMP gene can be used in vectors  
 CC (II) for expression in host cells and production or modulation of  
 CC production of fine chemicals, such as, an organic acid, a proteinogenic  
 CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,  
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty  
 CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a  
 CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins  
 CC (III) encoded by them are used for diagnosing the presence or activity of  
 CC Corynebacterium diptheriae in a subject. (I), (II), (III) or host cells  
 CC containing them are used to map genomes of organisms related to  
 CC C. glutamicum, identify and localise C. glutamicum sequences of interest,  
 CC in evolutionary studies. In determining C. glutamicum sequences required  
 CC for function, in modulating SMP protein activity, in modulating the  
 CC metabolism of sugars, and in modulating high-energy molecule production  
 CC in a cell (i.e. ATP, NADPH).  
 XX

SQ Sequence 2858 BP; 680 A; 789 C; 764 G; 625 T; 0 other;  
 Query Match 3.9%; Score 17; DB 22; Length 2858;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CGCGGCGCGACTTCGCG 23  
 DB 1887 CGCGGCGCGACTTCGCG 1903  
 RESULT 9  
 ABL18381/c  
 ID ABL18381 standard; DNA; 2957 BP.  
 XX ABL18381;  
 AC ABL18381;  
 XX 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6616.  
 KW Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ds.  
 XX Drosophila melanogaster.  
 XX WO200171042-A2.  
 PD 27-SEP-2001.  
 XX 23-MAR-2001; 2001WO-US09231.  
 XX 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 DR WPI; 2001-656860/75.  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX Claim 1; SEQ ID NO 6616; 21pp + Sequence Listing; English.  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01640-ABL16175) and the encoded proteins  
 CC (AAB57737-AB372072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 2957 BP; 717 A; 845 C; 736 G; 659 T; 0 other;  
 Query Match 3.9%; Score 17; DB 23; Length 2957;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 92 CGGTGGTGGCGGCGG 108  
 DB 1539 CGGTGGTGGCGGCGG 1523  
 RESULT 10  
 AAF71425  
 ID AAF71425 standard; DNA; 2967 BP.



XX AAF71425;  
 AC 30-APR-2001 (first entry)  
 DT  
 DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:131.  
 XX  
 XX Corynebacterium glutamicum; carbon metabolism and energy production;  
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;  
 KW fine chemical production; organic acid; proteinogenic amino acid;  
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
 KW carboxylate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 XX WO200100844-A2.  
 PN  
 XX  
 PD 04-JAN-2001.  
 XX  
 XX 23-JUN-2000; 2000WO-IB00943.  
 XX  
 XX 25-JUN-1999; 99US-0141031.  
 PR 08-JUL-1999; 99DE-1031412.  
 PR 08-JUL-1999; 99DE-1031413.  
 PR 08-JUL-1999; 99DE-1031419.  
 PR 08-JUL-1999; 99DE-1031420.  
 PR 08-JUL-1999; 99DE-1031424.  
 PR 08-JUL-1999; 99DE-1031428.  
 PR 08-JUL-1999; 99DE-1031431.  
 PR 08-JUL-1999; 99DE-1031433.  
 PR 08-JUL-1999; 99DE-1031434.  
 PR 08-JUL-1999; 99DE-1031436.  
 PR 08-JUL-1999; 99DE-1031562.  
 PR 08-JUL-1999; 99DE-1031634.  
 PR 09-JUL-1999; 99DE-1032180.  
 PR 09-JUL-1999; 99DE-1032227.  
 PR 09-JUL-1999; 99DE-1032230.  
 PR 09-JUL-1999; 99US-0143208.  
 PR 14-JUL-1999; 99DE-1032824.  
 PR 14-JUL-1999; 99DE-1032873.  
 PR 27-AUG-1999; 99DE-1040765.  
 PR 31-AUG-1999; 99US-0151572.  
 PR 03-SEP-1999; 99DE-1042076.  
 PR 03-SEP-1999; 99DE-1042079.  
 PR 03-SEP-1999; 99DE-1042086.  
 PR 03-SEP-1999; 99DE-1042087.  
 PR 03-SEP-1999; 99DE-1042088.  
 PR 03-SEP-1999; 99DE-1042095.  
 PR 03-SEP-1999; 99DE-1042123.  
 PR 03-SEP-1999; 99DE-1042125.  
 XX  
 XX (BADI ) BASF AG.  
 PA  
 XX  
 XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;  
 PI  
 XX  
 XX WPI: 2001-061975/07.  
 DR P-PSDB; AAB79308.  
 XX  
 XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar  
 PT metabolism and oxidative phosphorylation protein for production or  
 PT modulation of production of fine chemicals e.g. amino acids,  
 PT carbohydrates or enzymes  
 XX  
 XX Claim 3; Page 334-338; 1246pp; English.  
 PS  
 XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar  
 CC metabolism and oxidative phosphorylation (SMP) proteins given in  
 CC AAB79243 to AAB 79633 which are involved in carbon metabolism and  
 CC energy production. The C. glutamicum SMP gene can be used in vectors  
 CC (11) for expression in host cells and production or modulation of

CC production of fine chemicals, such as, an organic acid, a proteinogenic  
 CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,  
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty  
 CC acid, a diol, a carboxylate, an aromatic compound, a vitamin, a  
 CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins  
 CC (iii) encoded by them are used for diagnosing the presence or activity of  
 CC Corynebacterium diphtheriae in a subject. (i), (ii), (iii) or host cells  
 CC containing them are used to map genomes of organisms related to  
 CC C. glutamicum, identify and localise C. glutamicum sequences of interest,  
 CC in evolutionary studies, in determining SMP protein regions required  
 CC for function, in modulating SMP protein activity, in modulating the  
 CC metabolism of sugars, and in modulating high-energy molecule production  
 CC in a cell (i.e. ATP, NADPH).  
 XX  
 XX Sequence 2967 BP; 712 A; 819 C; 782 G; 654 T; 0 other;  
 SQ  
 Query Match 3.9%; Score 17; DB 22; Length 2967;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 7 CGCGCGCGACTCGCC 23  
 DB 1996 CGCGCGCGACTCGCC 2012  
 |||||  
 RESULT 11  
 AAC76210  
 ID AAC76210 standard; cDNA; 3026 BP.  
 XX  
 AC AAC76210;  
 XX  
 DT 08-FEB-2001 (first entry)  
 DE  
 DE Human ORFX ORF1765 polynucleotide sequence SEQ ID NO:3529.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunosuppressant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; systemic lupus erythematosus;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200058473-A2.  
 PN  
 XX  
 XX 05-OCT-2000.  
 PD  
 XX  
 XX 31-MAR-2000; 2000WO-US08621.  
 PF  
 XX  
 XX 31-MAR-1999; 99US-0127607.  
 PR 02-APR-1999; 99US-0127636.  
 PR 05-APR-1999; 99US-0127728.  
 PR 30-MAR-2000; 2000US-0540763.  
 XX  
 XX (CURA-) CUPAGEN CORP.  
 PA  
 XX  
 XX Shimkets RA, Leach M;  
 PI  
 XX WPI: 2000-60262/57.  
 DR P-PSDB; AAB42001.  
 XX  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -

```

XX PS Claim 5; Page 2695-2697; 5507pp; English.
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antiproliferative; antiparkinsonian; neotropic; neuroprotective;
CC osteoprotective; anticonvulsant; antirheumatic; immunosuppressive;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antihypertensive; antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease: to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX SQ Sequence 3026 BP; 619 A; 838 C; 955 G; 513 T; 1 other;

Query Match      3.98; Score 17; DB 21; Length 3026;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GGGCAGCGGTGGTGGC 101
DB 767 GGGCAGCGGTGGTGGC 783

RESULT 12
AAK80242/c
ID AAK80242 standard; DNA; 5282 BP.
AC AAK80242:
XX
XX 07-NOV-2001 (first entry)
XX Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:35054.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0215647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 14-JUL-2000; 2000US-0217456.
XX 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225256.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225271.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225457.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.

```



```

RESULT 14
ABLI4522
ID ABLI4522 standard; cDNA; 5440 BP.
XX
AC ABLI4522;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38048.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 38048; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABLI01840-ABLI30511), expressed DNA
CC sequences (ABLI01840-ABLI16175) and the encoded proteins
CC (ABB57737-ABB72072).
XX
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5440 BP; 1371 A; 1261 C; 1382 G; 1426 T; 0 other;

Query Match 3.9%; Score 17; DB 23; Length 5440;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CGGTGGTGGCGATGGCG 108
|||||
DB 2707 CGGTGGTGGCGATGGCG 2723

Search completed: November 30, 2002, 02:40:01
Job time : 298 secs

RESULT 15
ABLI18168
ID ABLI18168 standard; DNA; 5440 BP.
XX
AC ABLI18168;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5977.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;

```

```

KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 5977; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
CC sequences (ABLI01840-ABLI16175) and the encoded proteins
CC (ABB57737-ABB72072).
XX
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5440 BP; 1371 A; 1261 C; 1382 G; 1426 T; 0 other;

Query Match 3.9%; Score 17; DB 23; Length 5440;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CGGTGGTGGCGATGGCG 108
|||||
DB 2707 CGGTGGTGGCGATGGCG 2723

Search completed: November 30, 2002, 02:40:01
Job time : 298 secs

```



QY 62 TGGCGGTACCGCGGC 78  
DB 6414 TGGCGGTACCGCGGC 6430

RESULT 3  
US-08-991-789A-17  
; Sequence 17, Application US/08991789A  
; Patent No. 6225054  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; Smith, John M.  
; Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 292  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed IP Law Group  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,789A  
; FILING DATE: 11-Dec-1997  
; CLASSIFICATION: <unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 210121.419C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-08-991-789A-17

Query Match 3.6%; Score 16; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGCGC 108  
DB 172 GGTGGTGGCGATGCGC 187

RESULT 4  
US-08-991-789A-292  
; Sequence 292, Application US/08991789A  
; Patent No. 6225054  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; Smith, John M.  
; Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 292  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed IP Law Group  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle

STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/991,789A  
FILING DATE: 11-Dec-1997  
CLASSIFICATION: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 210121.419C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 292:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 292:  
US-08-991-789A-292

Query Match 3.6%; Score 16; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGCGC 108  
DB 172 GGTGGTGGCGATGCGC 187

RESULT 5  
US-09-062-451-17  
; Sequence 17, Application US/09062451  
; Patent No. 6344550  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Smith, John M.  
; APPLICANT: Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 297  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/062,451  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.419C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-062-451-17
;
Query Match 3.6%; Score 16; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTGGTGGCGATGCG 108
Db 172 GGTGGTGGCGATGCG 187

RESULT 6
US-09-598-326-17
; Sequence 17, Application US/09598326
; Patent No. 6423496
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; Smith, John M.
; Reed, Steven G.
;
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
;
NUMBER OF SEQUENCES: 247
;
CORRESPONDENCE ADDRESS:
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,326
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-598-326-17
;
Query Match 3.6%; Score 16; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTGGTGGCGATGCG 108
Db 172 GGTGGTGGCGATGCG 187

RESULT 7
US-09-280-116-34
; Sequence 34, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: aspartyl proteases
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(393)
; OTHER INFORMATION: n = a, t, c or g
; US-09-280-116-34
;
Query Match 3.6%; Score 16; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCGCGCGCGCGCA 16
Db 6 CGTCCGCGCGCGCGCA 21

RESULT 8
US-08-901-306-1
; Sequence 1, Application US/08901306
; Patent No. 5955319
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: BREME, Umberto
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: LOMOVSKAYA, Natasha
; APPLICANT: FONSTEIN, Leonid
; APPLICANT: OTTEN, Sharee
; APPLICANT: HUTCHINSON, Charles R.
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; FILE REFERENCE: 1615-7003
; CURRENT APPLICATION NUMBER: US/08/901,306
; CURRENT FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Streptomyces peucetius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(864)
; US-08-901-306-1
;
Query Match 3.6%; Score 16; DB 2; Length 864;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCGCGCGCGCGCA 16
Db 719 CGTCCGCGCGCGCGCA 734

RESULT 9
US-09-180-271-1
; Sequence 1, Application US/09180271
; Patent No. 6210930
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: LOMOVSKAYA, Natalia
; APPLICANT: FONSTEIN, Leonid
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: HUTCHINSON, C. Richard
```

```
; APPLICANT: OTTEN, Sharee L.
; APPLICANT: BREME, Umberto
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,271
; FILING DATE: 14-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03938
; FILING DATE: 05-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/901,306
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/812,412
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P1615-8010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..861
; US-09-180-271-1
;
; Query Match 3.6%; Score 16; DB 4; Length 864;
; Best Local Similarity 100.0%; Pred. No. 8.6;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 CGTCCGCGCGCGCGCA 16
Db 719 CGTCCGCGCGCGCGCA 734
;
RESULT 10
US-09-901-306-3
; Sequence 3, Application US/08901306
; Patent No. 595319
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: BREME, Umberto
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: LOMOVSKAYA, Natasha
; APPLICANT: FONSTEIN, Leonid
; APPLICANT: OTTEN, Sharee
; APPLICANT: HUTCHINSON, Charles R.
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; FILE REFERENCE: 1615-7003
; CURRENT APPLICATION NUMBER: US/08/901,306
; CURRENT FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 5
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Streptomyces peucetius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(255)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1219)..(1569)
; US-08-901-306-3
;
; Query Match 3.6%; Score 16; DB 2; Length 1569;
; Best Local Similarity 100.0%; Pred. No. 8.7;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 CGTCCGCGCGCGCGCA 16
Db 970 COTCCGCGCGCGCGCA 985
;
RESULT 11
US-09-180-271-3
; Sequence 3, Application US/09180271
; Patent No. 6210930
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: LOMOVSKAYA, Natalia
; APPLICANT: FONSTEIN, Leonid
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: HUTCHINSON, C. Richard
; APPLICANT: OTTEN, Sharee L.
; APPLICANT: BREME, Umberto
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,271
; FILING DATE: 14-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03938
; FILING DATE: 05-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/901,306
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/812,412
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P1615-8010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```



```
; MOLECULE TYPE: DNA
US-09-180-271-3

Query Match          3.6%; Score 16; DB 4; Length 1569;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCGCGCGCGGCGCA 16
    |||||
Db 970 CGTCGCGCGGCGCA 985

RESULT 12
US-09-382-106-1
; Sequence 1, Application US/09382106
; Patent No. 6221831
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: Jiang, Xinhe
; APPLICANT: McDevitt, Damien
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: tkta
; FILE REFERENCE: GM10236
; CURRENT APPLICATION NUMBER: US/09/382,106
; CURRENT FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-382-106-1

Query Match          3.6%; Score 16; DB 4; Length 1998;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGGCGCGACTTCGCC 23
    |||||
Db 996 GCGGCGCGACTTCGCC 1011

RESULT 13
US-09-222-575-149
; Sequence 149, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yugi, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (359)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (384)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
```

```
; LOCATION: (402)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-222-575-149

Query Match          3.4%; Score 15; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCGACTTCGCCTTTT 27
    |||||
Db 226 CCGACTTCGCCTTTT 240

RESULT 14
US-08-086-428B-38
; Sequence 38, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,428B
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6649
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: S52
US-08-086-428B-38

Query Match          3.4%; Score 15; DB 1; Length 576;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 ATGTTTCAGGACATC 195
    |||||
Db 362 ATGTTTCAGGACATC 376

RESULT 15
US-08-468-570-38
; Sequence 38, Application US/08468570
```

```

; Patent No. 5871962
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R. H. AND
; APPLICANT: PORCELL, R. H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,570
; FILING DATE: 6-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-40700S1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 759-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homosapiens
; INDIVIDUAL ISOLATE: S52
; US-08-468-570-38

Query Match 3.4%; Score 15; DB 2; Length 576;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 ATGTTTCAGGACATC 195
Db 362 ATGTTTCAGGACATC 376

Search completed: November 30, 2002, 02:40:59
Job time : 67 secs

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 01:37:17 : Search time 2081 Seconds  
(without alignments)  
3424.322 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtccgcgcgcgcgcactc.....ggaaatntagataaaaaant 440

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_esti:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_man:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	7.7	492	10 AW424591	AW424591 707018G10
2	34	7.7	646	14 BQ487045	BQ487045 1091050G1
3	34	7.7	974	11 AY108359	AY108359 Zea mays
4	26	5.9	491	9 AY948185	AY948185 603037E02
5	26	5.9	511	13 B1233723	B1233723 949032B03
6	24	5.5	531	10 AW925193	AW925193 WSL_76_E1

7	20	4.5	243	10	BE511251
8	20	4.5	408	9	AT756562
9	20	4.5	426	10	BE028394
10	20	4.5	428	13	BM305795
11	20	4.5	453	17	BH217843
12	20	4.5	508	10	BE522951
13	20	4.5	582	13	BM306218
14	20	4.5	583	10	BE553166
15	20	4.5	585	13	BM306028
16	20	4.5	604	13	BM305798
17	20	4.5	616	9	AT757288
18	20	4.5	991	11	AY104688
19	19	4.3	150	13	BI233722
20	19	4.3	287	9	AU088613
21	19	4.3	288	10	AW758690
22	19	4.3	359	9	AU065686
23	19	4.3	360	10	BE638916
24	19	4.3	412	12	BG039388
25	19	4.3	437	9	AT941641
26	19	4.3	501	12	BF221174
27	19	4.3	528	13	BM187966
28	19	4.3	545	14	BQ699897
29	19	4.3	558	14	BQ290844
30	19	4.3	600	10	BE511573
31	19	4.3	617	13	BM427811
32	19	4.3	649	13	BM332865
33	19	4.3	686	14	BQ654835
34	19	4.3	713	14	BQ391333
35	19	4.3	779	14	BQ700058
36	19	4.3	788	14	BQ698967
37	18	4.1	288	10	BB481838
38	18	4.1	325	13	BM153443
39	18	4.1	351	17	AQ843815
40	18	4.1	360	9	AJ465631
41	18	4.1	375	17	BH221877
42	18	4.1	375	17	BH222004
43	18	4.1	383	10	BE238451
44	18	4.1	401	10	BE125828
45	18	4.1	429	17	PL155L

ALIGNMENTS

RESULT 1  
AW424591  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES

AW424591  
707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea  
mays cDNA, mRNA sequence.  
AW424591.1 GI:6952523  
EST.  
Zea mays.  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACO  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 492)  
Walbot V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 707018 row: G column: 10.  
Location/Qualifiers  
1. 492  
/organism="Zea mays"

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

AW424591 707018G10.yl 707 - Mixed adult tissues from Walbot lab (SK) Zea

```

/cultivar="w23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
)"
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: tassel, kernel, silk, husk, root, leaf;
vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
BASE COUNT      89 a 146 g 106 t
ORIGIN

Query Match      7.7%; Score 34; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 CGCCTTTTCGTCGCCGGTCAGCGTCGGCGCTCC 53
|||||
Db 40 CGCCTTTTCGTCGCCGGTCAGCGTCGGCGCTCC 73
|||||

RESULT 2
BQ487045      646 bp mRNA linear EST 07-JUN-2002
LOCUS
DEFINITION
Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION
BQ487045
VERSION
BQ487045.1 GI:21331664
KEYWORDS
EST.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 646)
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
JOURNAL
REFERENCE
2 (bases 1 to 974)
Coe, E.C.
Direct Submission
TITLE
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
JOURNAL
FEATURES
Location/Qualifiers
source
1..974
/organism="Zea mays"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT      235 a 234 c 257 g 248 t
ORIGIN

Query Match      7.7%; Score 34; DB 11; Length 974;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 CGCCTTTTCGTCGCCGGTCAGCGTCGGCGCTCC 53
|||||
Db 45 CGCCTTTTCGTCGCCGGTCAGCGTCGGCGCTCC 78
|||||

RESULT 4
AI948185      491 bp mRNA linear EST 19-AUG-1999
LOCUS
DEFINITION
603037502.x1 603 - stressed root cDNA library from Wang/Bohnert lab
Zea mays cDNA, mRNA sequence.
ACCESSION
AI948185
VERSION
AI948185.1 GI:5740495
KEYWORDS
EST.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 491)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
JOURNAL
COMMENT
Department of Biological Sciences
Stanford University

Query Match      7.7%; Score 34; DB 14; Length 646;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 CGCCTTTTCGTCGCCGGTCAGCGTCGGCGCTCC 53
|||||

```

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227  
Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 603037 row: E column: 02.

Location/Qualifiers

#### FEATURES

source

1. 491  
/organism="Zea mays"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="603 - stressed root cDNA library from Wang/Bonnert lab"  
/tissue\_type="Seedling"  
/dev\_stage="salt stress"  
/lab\_host="E. coli XL Gold"  
/note="Organ: root; Vector: pBluescriptII SK(+ ) XR; Seeding stressed root cDNA library from Wang/Bonnert lab"  
2 others

#### BASE COUNT

ORIGIN

Query Match 5.9%; Score 26; DB 9; Length 491;  
Best Local Similarity 100.0%; Pred. No. 0.00071;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AGGCAGCGGTGTGGCGATGGCGT 109  
|||||  
Db 246 AGGCAGCGGTGTGGCGATGGCGT 271

#### RESULT 5

BI233723

LOCUS

DEFINITION 949032B03.v2 949 - Juvenile leaf and shoot cDNA from Steve Moose EST 11-JUL-2001

ACCESSION BI233723

VERSION BI233723

KEYWORDS EST, 1

SOURCE Zea mays.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS Walbot, V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 949032 row: B column: 03.

Location/Qualifiers

1. 511

/organism="Zea mays"

/cultivar="W64A"

/db\_xref="taxon:4577"

/clone\_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"

/tissue\_type="Immature leaf primordium and vegetative meristem"

/dev\_stage="4 stages from 3-13 days after imbibing"

/lab\_host="E. coli XL0LR"

/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site:1: EcoRI; Site:2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal

1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

#### BASE COUNT

ORIGIN

Query Match 5.9%; Score 26; DB 13; Length 511;  
Best Local Similarity 100.0%; Pred. No. 0.00071;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AGGCAGCGGTGTGGCGATGGCGT 109  
|||||  
Db 47 AGGCAGCGGTGTGGCGATGGCGT 72

#### RESULT 6

AW925193

LOCUS

DEFINITION WS1\_76\_E10.b1\_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.

ACCESSION AW925193

VERSION AW925193.1

KEYWORDS GI:8091019

SOURCE EST.

ORGANISM sorghum.

ORGANISM Sorghum bicolor

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

AUTHORS 1 (bases 1 to 531)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt

L.H.

An EST database from Sorghum: water-stressed plants

Unpublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude polyA, vector and regions

below Phred quality 16. The threshold for highest quality sequence

is 20.

Seq primer: JEN REV

High quality sequence stop: 458

POLYA-No.

Location/Qualifiers

1. 531

/organism="Sorghum bicolor"

/db\_xref="taxon:4558"

/clone\_lib="Water-stressed 1 (WS1)"

/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld. Vector: Lambda Zap; Site:1: XhoI; Site:2: EcoRI; The library was made from polyA RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

107 a 156 c 154 g 104 t

BASE COUNT

ORIGIN

Query Match 5.5%; Score 24; DB 10; Length 531;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GGCAGCGGTGTGGCGATGGCGT 109  
|||||  
Db 175 GGCAGCGGTGTGGCGATGGCGT 198

#### RESULT 7

BE511251

LOCUS BE511251 243 bp mRNA linear EST 07-AUG-2000  
 DEFINITION 946059A03.y1 946 - tassell primordium prepared by Schmidt lab zea  
 mays cDNA, mRNA sequence.  
 ACCESSION BE511251  
 VERSION BE511251.1 GI:9732499  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 243)  
 AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 University  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946059 row: A column: 03.  
 FEATURES  
 source  
 1..243  
 Location/Qualifiers  
 /organism="Zea mays"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /clone\_lib="946 - tassell primordium prepared by Schmidt  
 lab"  
 /tissue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to  
 inflorescence development"  
 /lab\_host="XLOU"  
 /note="Organ: tassels; Vector: HybriZAP; Site\_1: EcoRI;  
 Site\_2: XhoI; George Chuck dissected immature tassels  
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
 library in HybriZAP. Sample insert size range was 350 bp  
 to 3 Kb with a 1 Kb average."  
 BASE COUNT 29 a 93 c 74 g 47 t  
 ORIGIN  
 Query Match 4.5%; Score 20; DB 10; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 20 CGCCTTTTCGTCGCCGCGTC 39  
 ||||||||||||||||||  
 Db 16 CGCCTTTTCGTCGCCGCGTC 35  
 RESULT 8  
 A1756562 408 bp mRNA linear EST 18-JAN-2000  
 LOCUS A1756562  
 DEFINITION E18Ste02e09.y1 Elmeria M5-6 Merozoite stage Elmeria tenella cDNA  
 5', similar to SW:R141\_MAIZE P19950 40S RIBOSOMAL PROTEIN S14 ,,  
 mRNA sequence.  
 ACCESSION A1756562  
 VERSION A1756562.1 GI:5150285  
 KEYWORDS EST.  
 SOURCE Elmeria tenella.  
 ORGANISM Elmeria tenella.  
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Elmeriidae;  
 Elmeria.  
 REFERENCE 1 (bases 1 to 408)  
 AUTHORS Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T.,  
 Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen  
 M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey  
 N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson  
 Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and Sibley, D.  
 WashU-Merck Elmeria tenella project  
 Unpublished (1999)

COMMENT Contact: David Sibley, Ph.D.  
 WashU-Merck Elmeria tenella project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Contact David Sibley (toxeat@borcim.wustl.edu) for further  
 information relating to organism libraries, or clone availability.  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: 40RP from Gibco  
 High quality sequence stop: 393.  
 Location/Qualifiers  
 1..408  
 /organism="Elmeria tenella"  
 /strain="LS18"  
 /db\_xref="taxon:5802"  
 /clone\_lib="Elmeria M5-6 Merozoite stage"  
 /dev\_stage="Merozoite"  
 /lab\_host="SOLR E. coli"  
 /note="Vector: Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI  
 ; Merozoites were obtained from ceasal scrapings of  
 chickens infected with E. tenella. The library may  
 contain a small percentage of host or bacterial  
 contaminants. cDNA was synthesized from poly mRNA using  
 an oligo-dT primer containing a XhoI site. Following  
 second strand synthesis, EcoRI adapters were ligated to  
 the cDNA and products were size-selected on Sephacryl  
 S500. cDNAs were digested with EcoRI/XhoI and cloned into  
 lambda zap II (Stratagene). Clones were converted to  
 phagemids by mass excision using EXAssist helper phage and  
 SOLR cells (Stratagene). Insert sizes range from 0.7-1.5  
 kb."  
 BASE COUNT 73 a 156 c 129 g 50 t  
 ORIGIN  
 Query Match 4.5%; Score 20; DB 9; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 60 CGTGGCGGTCACCGCGGCA 79  
 ||||||||||||||||||  
 Db 138 CGTGGCGGTCACCGCGGCA 157  
 RESULT 9  
 BE028394 426 bp mRNA linear EST 07-JUN-2000  
 LOCUS BE028394  
 DEFINITION E18Ste77f06.y1 Elmeria M5-6 Merozoite stage subtracted Elmeria  
 tenella cDNA 5', similar to SW:R141\_MAIZE P19950 40S RIBOSOMAL  
 PROTEIN S14 , mRNA sequence.  
 ACCESSION BE028394  
 VERSION BE028394.1 GI:8321824  
 KEYWORDS EST.  
 SOURCE Elmeria tenella.  
 ORGANISM Elmeria tenella.  
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Elmeriidae;  
 Elmeria.  
 REFERENCE 1 (bases 1 to 426)  
 AUTHORS Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T.,  
 Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen  
 M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey  
 N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson  
 Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and Sibley, D.  
 WashU-Merck Elmeria tenella project  
 Unpublished (1999)  
 TITLE JOURNAL  
 COMMENT Contact: David Sibley, Ph.D.  
 WashU-Merck Elmeria tenella project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 423.  
Location/Qualifiers

#### FEATURES

source

```
1. .426
/organism="Eimeria tenella"
/strain="IS18"
/db_xref="taxon:5802"
/clone_lib="Eimeria M5-6 Merozoite stage subtracted"
/dev_stage="Merozoite"
/lab_host="SOLR E. coli"
/note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2: XhoI
; Merozoites were obtained from ceacal scrapings of
chickens infected with E. tenella. cDNA was synthesized
from poly mRNA using an oligo-dT primer containing a XhoI
site. Following second strand synthesis, EcoRI adapters
were ligated to the cDNA and products were size-selected
on Sephacryl S500. The cDNAs were ligated to EcoRI/XhoI
prepared lambda ZAPII(Stratagene). Clones were converted
to phagemids by mass excision using ExAssist helper phage
and E.coli SOLR cells (Stratagene). Insert sizes range
from 0.7-1.5kb. The library may contain a small percentage
of host or bacterial contaminants. Clones were selected by
negative hybridization against a pool of over-represented
ESTs (NP=10, from 1506 previous reads)."
BASE COUNT      76 a 153 c 141 g 56 t
ORIGIN
```

Query Match 4.5%; Score 20; DB 10; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 CGTGGCGTCACCGCGGCA 79

Db 67 CGTGGCGTCACCGCGGCA 86

RESULT 10

BM305795

LOCUS

DEFINITION

ETESTee40f01.y1 Eimeria tenella M5-6 cDNA Neg Selected Eimeria

tenella cDNA 5' similar to SW:RS14\_CAEEL P48150 PROBABLE 40S

RIBOSOMAL PROTEIN S14. [1] ; mRNA sequence.

BM305795

BM305795.1 GI:18037501

EST.

Eimeria tenella.

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;

Eimeria.

1 (bases 1 to 428)

Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,

Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen

M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Tape,D., Harvey

N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson

Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D.

WashU-Merck Eimeria tenella project

Unpublished (1999)

Contact: David Sibley, Ph.D.

WashU-Merck Eimeria tenella project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Contact David Sibley (toxoest@borcim.wustl.edu) for further

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco

High quality sequence stop: 367.

Location/Qualifiers

1. .428

/organism="Eimeria tenella"

```
/strain="IS18"
/db_xref="taxon:5802"
/clone_lib="Eimeria tenella M5-6 cDNA Neg Selected"
/dev_stage="Merozoite"
/lab_host="DH10B (GENEHOG, E.coli HS996)"
/note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2: XhoI
; Merozoites were obtained from ceacal scrapings of
chickens infected with E. tenella. cDNA was synthesized
from poly mRNA using an oligo-dT primer containing a XhoI
site. Following second strand synthesis, EcoRI adapters
were ligated to the cDNA and products were size-selected
on Sephacryl S500. The cDNAs were ligated to EcoRI/XhoI
prepared lambda ZAPII(Stratagene). Clones were converted
to phagemids by mass excision using ExAssist helper phage
and E.coli SOLR cells (Stratagene). Clones were selected
by negative hybridization against a pool of
over-represented ESTs (NP=10, from 1506 previous reads),
and transformed to DH10B (GENEHOGS, STRATAGENE). The
library may contain a small percentage of host or
bacterial contaminants."
```

BASE COUNT 66 a 128 c 154 g 80 t

ORIGIN

Query Match 4.5%; Score 20; DB 13; Length 428;

Best Local Similarity 100.0%; Pred. No. 2.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 CGTGGCGTCACCGCGGCA 79

Db 347 CGTGGCGTCACCGCGGCA 366

RESULT 11

BM217843

LOCUS

DEFINITION

1006060C11.y1 1006 - RescueMu Grid G Zea mays genomic, DNA

sequence.

BM217843

BM217843.1 GI:16809899

GSS.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Ze mays.

Mu elements insert preferentially into transcription units. For more information on Rescuem, go to the web site 'www.zandb.iastate.edu' and follow the links for 'Rescuem', 'GridC' was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and SglI, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 58 a 150 c 133 g 112 t  
ORIGIN

Query Match 4.5%; Score 20; DB 17; Length 453;

Best Local Similarity 100.0%; Pred. No. 2.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AGGCGAGGAGCGCGTGT 98  
|||||

Db 109 AGGCGAGGAGCGCGTGT 128

# RESULT 12

BE552951

LOCUS 946087G06.y1 946 - tassal primordium prepared by Schmidt lab Zea  
mays cDNA, mRNA sequence.

DEFINITION BE552951

ACCESSION BE552951.1 GI:9794643

VERSION EST.

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; PACC  
clade: Panicoidae; Andropogoneae; Zea.

TITLE 1 (bases 1 to 508)

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford

UNPUBLISHED (1999)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946087 row: G column: 06.

Location/Qualifiers

1..508

/organism="Zea mays"

/cultivar="OH43"

/db\_xref="taxon:4577"

/clone\_lib="946 - tassal primordium prepared by Schmidt

lab"

/tissue\_type="tassels"

/dev\_stage="just after the transition from vegetative to

inflorescence development"

/lab\_host="XLOLR"

/note="Organ: tassels; Vector: HybriZAP; Site.1: EcoRI;

Site.2: XhoI; George Chuck dissected immature tassels

between 1mm and 3mm. Sharon Stanfield prepared the cDNA

library in HybriZAP. Sample insert size range was 350 bp

to 3 kb with a 1 kb average."

BASE COUNT 98 a 143 c 149 g 118 t

# ORIGIN

Query Match 4.5%; Score 20; DB 10; Length 508;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AGGCGAGGAGCGCGTGT 98

|||||

Db 59 AGGCGAGGAGCGCGTGT 78

# RESULT 13

BM306218

LOCUS

DEFINITION

EMERIIDAE

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

FEATURES

source

BM306218 582 bp mRNA linear EST 02-JAN-2002  
EMERIIDAE2607.y1 Eimeria tenella M5-6 cDNA Neg Selected Eimeria  
tenella cDNA 5' similar to SW:R141\_MAZE P19950 40S RIBOSOMAL  
PROTEIN S14 ; mRNA sequence.

ACCESSION BM306218

VERSION GI:18037924

KEYWORDS EST.

SOURCE Eimeria tenella.

ORGANISM Eimeria tenella.

REFERENCE Eukaryota: Alveolata: Apicomplexa: Coccidia; Eimeriida: Eimeriidae;

1 (bases 1 to 582)

Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T.,

Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen

M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey

N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson

Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and Sibley, D.

WashU-Merck Eimeria tenella project

Unpublished (1999)

CONTACT: David Sibley, Ph.D.

WashU-Merck Eimeria tenella project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

CONTACT David Sibley (toxest@borcim.wustl.edu) for further

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco

High quality sequence stop: 412.

Location/Qualifiers

1..582

/organism="Eimeria tenella"

/db\_xref="taxon:5802"

/clone\_lib="Eimeria tenella M5-6 cDNA Neg Selected"

/dev\_stage="DH10B (GENEGOG, E.coli HS996)"

/lab\_host="Bluescript SK-; Site.1: EcoRI; Site.2: XhoI

; Merzotites were obtained from cecal scrapings of

chickens infected with E. tenella. cDNA was synthesized

from poly mRNA using an oligo-dT primer containing a XhoI

site. Following second strand synthesis, EcoRI adapters

were ligated to the cDNA and products were size-selected

on Sephadryl S500. The cDNAs were ligated to EcoRI/XhoI

prepared lambda ZAPII(Stratagene). Clones were converted

to phagemids by mass excision using ExAssist helper phage

and E.coli SOLR cells (Stratagene). Clones were selected

by negative hybridization against a pool of

over-represented ESTs (N>=10, from 1506 previous reads),

and transformed to DH10B (GENEGOGS, STRATAGENE). The

library may contain a small percentage of host or

bacterial contaminants."

BASE COUNT 89 a 189 c 212 g 91 t

1 others

Query Match 4.5%; Score 20; DB 13; Length 582;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CGTGGCGCTGACGGCGCA 79

|||||

Db 339 CGTGGCGCTGACGGCGCA 358

# RESULT 14

BE553166

LOCUS

DEFINITION

BE553166 583 bp mRNA linear EST 10-AUG-2000  
946089H09.y1 946 - tassal primordium prepared by Schmidt lab Zea  
mays cDNA, mRNA sequence.



```

ACCESSION   BE553166
VERSION     BE553166.1  GI:9794858
KEYWORDS    EST.
SOURCE      zea mays.
ORGANISM    zea mays.

REFERENCE   1  (bases 1 to 583)
AUTHORS     Walbot,V.
TITLE       Maize ESTs from various cDNA libraries sequenced at Stanford
COMMENT     Unpublished (1999)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946089 row: H column: 09.
            Location/Qualifiers
              1..583
                /organism="Zea mays"
                /cultivar="OH43"
                /db_xref="taxon:4577"
                /clone_lib="946 - tassels primordium prepared by Schmidt
                lab"
                /tissue_type="tassels"
                /dev_stage="just after the transition from vegetative to
                inflorescence development"
                /lab_host="XLOLR"
                /note="Organ: tassels; Vector: HybridZAP; Site.1: EcoRI;
                Site.2: XhoI; George Chuck dissected immature tassels
                between lmm and 3mm. Sharon Stanfield prepared the cDNA
                library in HybridZAP. Sample insert size range was 350 bp
                to 3 Kb with a 1 Kb average."
                114 a 157 c 175 g 137 t

BASE COUNT  114 a 157 c 175 g 137 t

ORIGIN
Query Match      4.5%; Score 20; DB 10; Length 583;
Best Local Similarity 100.0%; Pred.No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  20  CGCCTTTTCGTCGCCGCGPC 39
      |||||||
Db    6  CGCCTTTTCGTCGCCGCGPC 25

RESULT 15
LOCUS      BM306028
DEFINITION ETEESTee23g03.y1 Eimeria tenella M5-6 cDNA Neg Selected Eimeria
            tenella cDNA 5', similar to SW:R141_MAIZE P19950 40S RIBOSOMAL
            PROTEIN S14 ;, mRNA sequence.
ACCESSION  BM306028
VERSION    BM306028.1  GI:18037734
KEYWORDS   EST.
SOURCE     Eimeria tenella.
ORGANISM   Eimeria tenella.
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
            Eimeria
            1 (bases 1 to 585)
            Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
            Martin,D., Wyllie,F., Underwood,K., Steptoe,M., Theising,B., Allen
            ,M., Bowers,I., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey
            ,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson
            ,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D.
            WashU-Merck Eimeria tenella project
            Unpublished (1999)
            Contact: David Sibley, Ph.D.
            WashU-Merck Eimeria tenella project
            Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Contact David Sibley (toxoest@porcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 378.
Location/Qualifiers
  1..585
    /organism="Eimeria tenella"
    /strain="is18"
    /db_xref="taxon:5802"
    /clone_lib="Eimeria tenella M5-6 cDNA Neg Selected"
    /dev_stage="Merzoite"
    /lab_host="DH10B (GENEHOG, E.coli HS996)"
    /note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2: XhoI
    ; Merzoites were obtained from ceacal scrapings of
    chickens infected with E. tenella. cDNA was synthesized
    from poly mRNA using an oligo-dT primer containing a XhoI
    site. Following second strand synthesis, EcoRI adapters
    were ligated to the cDNA and products were size-selected
    on Sephacryl S500. The cDNAs were ligated to EcoRI/XhoI
    prepared lambda ZAPII(Stratagene). Clones were converted
    to phagemids by mass excision using EXAssist helper phage
    and E.coli SOLR cells (Stratagene). Clones were selected
    by negative hybridization against a pool of
    over-represented ESTs (N>=10, from 1506 previous reads),
    and transformed to DH10B (GENEHOGS, STRATAGENE). The
    library may contain a small percentage of host or
    bacterial contaminants."
    90 a 188 c 208 g 95 t 4 others

BASE COUNT  90 a 188 c 208 g 95 t 4 others

ORIGIN
Query Match      4.5%; Score 20; DB 13; Length 585;
Best Local Similarity 100.0%; Pred.No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  60  CGTGGCGGTACCGCGCGCA 79
      |||||||
Db    354  CGTGGCGGTACCGCGCGCA 373

Search completed: November 30, 2002, 04:01:12
Job time : 2095 secs

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 02:35:57 ; Search time 56 Seconds

(Without alignments)  
3025.907 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtcgcgcgcgcgcacttc.....ggaatntagataaaaaant 440

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 341543 seqs, 192557720 residues

Word size : 0

Total number of hits satisfying chosen parameters: 583086

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US05\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US05\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	5.9	216	10	US-09-923-876-28
2	18	4.1	255	10	US-09-923-876-6319
3	17	3.9	761	12	US-10-062-254-55
4	17	3.9	1612	12	US-10-062-254-57
5	16	3.6	250	10	US-09-878-574-10592
6	16	3.6	286	9	US-09-924-400-17
7	16	3.6	286	10	US-09-810-936-17
8	16	3.6	286	10	US-09-429-755-17
9	16	3.6	900	10	US-09-815-242-6108
10	16	3.6	939	9	US-09-938-842A-2421
11	16	3.6	1866	10	US-09-802-874-1
12	16	3.6	1870	9	US-09-981-353-109
13	16	3.6	1998	10	US-09-815-242-7695
14	16	3.6	2000	9	US-09-938-842A-4602
15	16	3.6	2208	10	US-09-815-242-7991
16	16	3.6	3119	10	US-09-867-701-10873
17	16	3.6	3123	10	US-09-912-020-122
18	16	3.6	3123	10	US-09-815-242-6106
19	16	3.6	13029	10	US-09-815-242-4052

c	20	16	3.6	20633	10	US-09-070-927A-276	Sequence 276, Ap
	21	15	3.4	36	10	US-09-973-322-15	Sequence 15, Appl
c	22	15	3.4	203	10	US-09-294-093B-4713	Sequence 4713, Ap
c	23	15	3.4	276	10	US-09-294-093B-5682	Sequence 5682, Ap
c	24	15	3.4	281	10	US-09-294-093B-5703	Sequence 5703, Ap
c	25	15	3.4	283	10	US-09-294-093B-4681	Sequence 4681, Ap
c	26	15	3.4	288	10	US-09-294-093B-1526	Sequence 1526, Ap
c	27	15	3.4	296	10	US-09-294-093B-6090	Sequence 6090, Ap
c	28	15	3.4	300	10	US-09-974-300-8146	Sequence 8146, Ap
c	29	15	3.4	301	10	US-09-864-761-24056	Sequence 24056, A
c	30	15	3.4	402	10	US-09-974-300-1897	Sequence 1897, Ap
c	31	15	3.4	439	10	US-09-604-287A-149	Sequence 149, App
c	32	15	3.4	439	10	US-09-339-338-149	Sequence 149, App
c	33	15	3.4	439	12	US-10-007-805-149	Sequence 149, App
c	34	15	3.4	472	10	US-09-974-300-6336	Sequence 6336, Ap
c	35	15	3.4	556	10	US-09-864-761-7326	Sequence 7326, Ap
c	36	15	3.4	597	9	US-09-727-855B-6	Sequence 6, Appl
c	37	15	3.4	817	10	US-09-925-301-165	Sequence 165, App
c	38	15	3.4	1035	9	US-09-712-363-83	Sequence 83, Appl
c	39	15	3.4	1109	9	US-09-938-842A-3333	Sequence 3333, Ap
c	40	15	3.4	1119	10	US-09-921-992-3	Sequence 3, Appl
c	41	15	3.4	1191	10	US-09-741-669-223	Sequence 223, App
c	42	15	3.4	1311	10	US-09-790-264-31	Sequence 31, Appl
c	43	15	3.4	1440	10	US-09-790-264-40	Sequence 40, Appl
c	44	15	3.4	1686	10	US-09-812-079A-1	Sequence 1, Appl
c	45	15	3.4	1773	10	US-09-815-242-4044	Sequence 4044, Ap

#### ALIGNMENTS

RESULT 1  
US-09-923-876-28  
; Sequence 28, Application US/09923876  
; Patent No. US20020013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Kamigaki, Laura Y. (Ico)  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/085,331  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 28  
; LENGTH: 216  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700142447H1  
US-09-923-876-28  
Query Match 5.9%; Score 26; DB 10; Length 216;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 AGCCGACGGCGTGGCGGCGCGT 109  
Db 3 AGCCGACGGCGTGGCGGCGCGT 28  
RESULT 2  
US-09-923-876-6319  
; Sequence 6319, Application US/09923876  
; Patent No. US20020013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.

```

; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 6319
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458871H1
US-09-923-876-6319

Query Match          4.1%; Score 18; DB 10; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 86 GGCAGCGGTGGTGGCGA 103
DB 169 GCCAGCGGTGGTGGCGA 186

RESULT 3
; Sequence 55, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Oryza sativa

```

```

; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 55
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (69)
; NAME/KEY: unsure
; LOCATION: (73)
US-10-062-254-55

Query Match          3.9%; Score 17; DB 12; Length 761;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 CGTCACCGCGGCAGGC 82
DB 84 CGTCACCGCGGCAGGC 100

RESULT 4
; Sequence 57, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Oryza sativa

```

US-10-062-254-57

Query Match 3.9%; Score 17; DB 12; Length 1612;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 GCTCACCAGCGGCGAGCG 82  
DB 91 GCTCACCAGCGGCGAGCG 107

## RESULT 5

US-09-878-574-10532  
; Sequence 10592, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 10592  
; LENGTH: 250  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700966847H1  
US-09-878-574-10592

Query Match 3.6%; Score 16; DB 10; Length 250;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 GCGGGTGTGGCGGATG 105  
DB 162 GCGGGTGTGGCGGATG 177

## RESULT 6

US-09-924-400-17  
; Sequence 17, Application US/09924400  
; Patent No. US20020165371A1  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Smith, John M.  
; APPLICANT: Mishler, Lynda E.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Deng, Ta

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.419C12  
; CURRENT APPLICATION NUMBER: US/09/924,400  
; CURRENT FILING DATE: 2001-08-07  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-924-400-17

Query Match 3.6%; Score 16; DB 10; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3.6%; Score 16; DB 9; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGGCG 108  
DB 172 GGTGGTGGCGATGGCG 187

## RESULT 7

US-09-810-936-17  
; Sequence 17, Application US/09810936  
; Patent No. US20020068285A1  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Smith, John M.  
; APPLICANT: Mishler, Lynda E.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Day, Craig H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.419C11  
; CURRENT APPLICATION NUMBER: US/09/810,936  
; CURRENT FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-810-936-17

Query Match 3.6%; Score 16; DB 10; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGGCG 108  
DB 172 GGTGGTGGCGATGGCG 187

## RESULT 8

US-09-429-755-17  
; Sequence 17, Application US/09429755A  
; Patent No. US20020111467A1  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Smith, John M.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Mishler, Lynda E.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.419C6  
; CURRENT APPLICATION NUMBER: US/09/429,755A  
; CURRENT FILING DATE: 1999-10-28  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-429-755-17

Query Match 3.6%; Score 16; DB 10; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGGC 108  
DB 172 GGTGGTGGCGATGGC 187

## RESULT 9

US-09-938-842A-6108  
; Sequence 6108, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6108  
; LENGTH: 900  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(900)  
US-09-938-842A-6108

Query Match 3.6%; Score 16; DB 10; Length 900;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CGGTGGTGGCGATGGC 107  
DB 189 CGGTGGTGGCGATGGC 204

## RESULT 10

US-09-938-842A-2421/c  
; Sequence 2421, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS. TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME AND METHODS OF USE  
; FILE REFERENCE: SGP1500-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2421  
; LENGTH: 939  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2421

Query Match 3.6%; Score 16; DB 9; Length 939;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 GCGTGGTGGCGATGG 106  
DB 628 GCGTGGTGGCGATGG 613

## RESULT 11

US-09-802-674-1/c  
; Sequence 1, Application US/09802674  
; Patent No. US20020042088A1  
; GENERAL INFORMATION:  
; APPLICANT: Macina, Roberto A  
; APPLICANT: Piderit, Alejandra  
; APPLICANT: Sun, Yongming  
; TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and  
; TITLE OF INVENTION: Treating Gastrointestinal Cancer  
; FILE REFERENCE: DEX-0142  
; CURRENT APPLICATION NUMBER: US/09/802,674  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,061  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1866  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-802-674-1

Query Match 3.6%; Score 16; DB 10; Length 1866;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GGCAGCGGTGGTGGC 101  
DB 736 GGCAGCGGTGGTGGC 721

## RESULT 12

US-09-981-353-109/c  
; Sequence 109, Application US/09981353  
; Patent No. US20020160382A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; APPLICANT: Jones, David A.  
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
; FILE REFERENCE: PA-0038 US  
; CURRENT APPLICATION NUMBER: US/09/981,353  
; CURRENT FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PERL Program  
; SEQ ID NO 109  
; LENGTH: 1870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20020160382A1 273879C81

Direct Submission									
Submitted (16-MAR-2001) Salk Institute Genomic Analysis Laboratory									
(Signal), Plant Biology Laboratory, The Salk Institute for									
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,									
USA									
On Mar 16, 2001 this sequence version replaced gi:11762327.									
RIKEN Genomic Sciences Center (GSC) members carried out the									
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN									
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,									
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,									
Hayashizaki,Y. and Shinozaki,K.									
The Salk, Stanford, PGSC (SSP) Consortium members carried out the									
sequencing and annotation of the RAFL cDNAs: Shinn,P., Chen,H.,									
Cheuk,R., Kim,C.J., Koesema,B., Meyers,M.C., Tracy,S.E., Banh,J.,									
Bowser,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G.,									
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,									
Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A.,									
Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A.,									
and Ecker,J.R.									
Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to									
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)									
contributed equally to this work as PIs.									
FEATURES									
source									
1..879									
/organism="Arabidopsis thaliana"									
/db_xref="taxon:3702"									
/chromosome="1"									
/clone="000C19F01(S63)"									
/note="ecotype: Columbia"									
1..879									
/gene="Atlg27450/F17L21_25"									
1..51									
/gene="Atlg27450/F17L21_25"									
52..603									
/note="adenine phosphoribosyltransferase 1, APR"									
/codon_start=1									
/product="Atlg27450"									
/db_xref="GI:11762328"									
/protein_id="AAG40397.1"									
/translation="MATEDVDQPRKIASSIRVDPKPGIMFQDITLLDTEAF									
KDTIALVFRYDKGISVWAGVEARCFIFGPALATFGKVFPMRKPGLKGVISE									
VSYLEGTDTIEHMGVPEGRERAIIDDLATGTGLAAIRLLERVGVKIVECACVIE									
LPELKGKELGETSLFVLVKSA"									
604..879									
/gene="Atlg27450/F17L21_25"									
BASE COUNT 234 a 153 c 221 g 271 t									
ORIGIN									
Query Match 19.7%; Score 86.6; DB 8; Length 879;									
Best Local Similarity 55.7%; Pred. No. 8.7e-10;									
Matches 180; Conservative 0; Mismatches 139; Indels 4; Gaps 3;									
Qy 115 GATGCGCGCTGGCGGNGATCGNCTCTTCATCCGCTTATCCCAAGCCCA 174									
Db 73 GATCCAGAAATCGTAGATTCCTTCCCAATAGATCATCCGCTTCCCAACCA 132									
Qy 175 GGGATNATGTTTCAGGACATCANGANGNTGNTGTCATCCCAAGCGCTCCGTGCACAC 234									
Db 133 GGAATCATGTTTTCAGGACATCAAGACGCTTCTTCTCGACACATGAGGCTTTTAAGGACT 192									
Qy 235 ATATACCATTTTGTCAAGCGGTACAGGACCAAGGATACACCTGGAANTAGAGATTAA 294									
Db 193 ATTGCTTTGTTTGTATAGATACAAAGATAAAGGCATATCTGTTC-ATGCAAGGTGTGA 251									
Qy 295 AGCTAGAGGNTTCANTTTCGGAACACACTANNCTTTANAANNAATTTGGTCAAAATNGGTG 354									
Db 252 AGCTAGAGGTTTCATTTTGGCCCTCCCTATTGCGCTTG--GCTATTGGTGCCAAATTTGTT 309									
Qy 355 NCNATTTCAGGACGACNNATNAGTTCGCANGCNAATGATTTTNGAATATNGAATTTTNG 414									
TITLE									
JOURNAL									
BASE COUNT 204 a 123 c 189 g 213 t									
ORIGIN									
Query Match 19.7%; Score 86.6; DB 8; Length 729;									
Best Local Similarity 55.7%; Pred. No. 8.4e-10;									
Matches 180; Conservative 0; Mismatches 139; Indels 4; Gaps 3;									
Qy 115 GATGCGCGCTGGCGGNGATCGNCTCTTCATCCGCTTATCCCAAGCCCA 174									
Db 39 GATCCAGAAATCGTAGATTCCTTCCCAATAGATCATCCGCTTCCCAACCA 98									
Qy 175 GGGATNATGTTTCAGGACATCANGANGNTGNTGTCATCCCAAGCGCTCCGTGCACAC 234									
Db 99 GGAATCATGTTTTCAGGACATCAAGACGCTTCTTCTCGACACTGAGGCTTTTAAGGACT 158									
Qy 235 ATATACCATTTTGTCAAGCGGTACAGGACCAAGGATACACCTGGAANTAGAGATTAA 294									
Db 159 ATTGCTTTGTTTGTATAGATACAAAGATAAAGGCATATCTGTTC-ATGCAAGGTGTGA 217									
Qy 295 AGCTAGAGGNTTCANTTTCGGAACACACTANNCTTTANAANNAATTTGGTCAAAATNGGTG 354									
Db 218 AGCTAGAGGTTTCATTTTGGCCCTCCCTATTGCGCTTG--GCTATTGGTGCCAAATTTGTT 275									
Qy 355 NCNATTTCAGGACGACNNATNAGTTCGCANGCNAATGATTTTNGAATATNGAATTTTNG 414									
Db 276 CCA-TCAGGAAGCCCAAGGACTACCTGGGNAAGTTATTTCCGAGGACTATTCGTTGGA 334									
Qy 415 GAATNGGAATNTAGATAAAA 437									
Db 335 GTATGGAACGATACGATTGTGA 357									
RESULT 5									
AF325045									
LOCUS									
DEFINITION									
Arabidopsis thaliana Atlg27450 (Atlg27450/F17L21_25) mRNA, complete									
cds.									
AF325045									
AF325045.2 GI:13358234									
FLI.CDNA.									
Arabidopsis thaliana.									
Arabidopsis thaliana.									
Arabidopsis thaliana.									
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots;									
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.									
1 (bases 1 to 879)									
REFERENCE									
AUTHORS									
Shinn,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C.,									
Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D.,									
Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,									
Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H.,									
Southwick,A., Toriumi,M., Yamada,K., Yu,G., Davis,R.W.,									
Theologis,A. and Ecker,J.R.									
Arabidopsis cDNA clones									
Unpublished									
2 (bases 1 to 879)									
REFERENCE									
AUTHORS									
Shinn,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C.,									
Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D.,									
Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,									
Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H.,									
Southwick,A., Toriumi,M., Yamada,K., Yu,G., Davis,R.W.,									
Theologis,A. and Ecker,J.R.									
Direct Submission									
Submitted (30-NOV-2000) Salk Institute Genomic Analysis Laboratory									
(Signal), Plant Biology Laboratory, The Salk Institute for									
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,									
USA									
3 (bases 1 to 879)									
REFERENCE									
AUTHORS									
Shinn,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C.,									
Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D.,									
Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,									
Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano									

RESULT 3  
 AY084300  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 AY084300 1036 bp mRNA linear PLN 21-JUN-2002  
 Arabidopsis thaliana clone 102971 mRNA, complete sequence.  
 AY084300  
 AY084300.1 GI:21403010  
 FLI.CDNA  
 thale cress.  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 1036)  
 Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N.,  
 Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.  
 Full-length messenger RNA sequences greatly improve genome  
 annotation  
 Genome Biol. (2002) In press  
 2 (bases 1 to 1036)  
 Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
 Feldmann,K.  
 Full-length cDNA from Arabidopsis thaliana  
 Unpublished  
 3 (bases 1 to 1036)  
 Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
 Feldmann,K.  
 Direct Submission  
 Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
 Malibu, CA 90265, USA  
 This clone sequence is one of 5,000 Ceres full-length cDNAs made  
 available to TIGR and Genbank. The following quality assessment of  
 this set was done by comparison with known proteins: two percent of  
 the clones are estimated to be 5'-truncated; less than one percent  
 are 3'-truncated; approximately two percent represent alternative  
 splice variants, including unspliced introns and spliced exons; one  
 percent may contain premature stop codons; five percent may have  
 frame shifts in a coding region. A sequence is considered to be  
 5'-truncated if it lacks the translation initiation start (ATG). A  
 sequence is considered to be 3'-truncated if it lacks the  
 C-terminal end of the encoded protein. Please note that these cDNA  
 sequences are derived from the WS or Laer ecotypes and therefore  
 may contain polymorphisms when compared to sequences from Col-0.  
 Genset carried out the library production and sequencing of the  
 full-length clones. Ceres, Inc. carried out the clustering of the  
 5' sequences, selection of clones, and sequence assembly.  
 Location/Qualifiers  
 1..1036  
 /organism="Arabidopsis thaliana"  
 /db\_xref="taxon:3702"  
 /clone="102971"  
 122..853  
 /codon\_start=1  
 /product="adenine phosphoribosyltransferase 1, APRT"  
 /protein\_id="FAM60891.1"  
 /db\_xref="GI:21536559"  
 /translation="MTIIISPLVSHRCLARAVPCNRLNNHRRAPPISRLSHNRST  
 TSLRFSARASRSEMYEDVDPRIAKTSIRVDPFKPGIMFQDITLLDTEAF  
 AKDTIALVDYRDKGISVAGVEARGFPGPIALAIKAKEVPMRKKLPKGVIS  
 EYSLEYGDTIEHVGAVGERAIIDDLIATGTTAAAIRLLRERGVKIVEACV  
 IEPLKGEKLGETSLFLVLRSA"  
 BASE COUNT 261 a 220 c 235 g 320 t  
 ORIGIN  
 Query Match 20.1%; Score 88.4; DB 8; Length 1036;  
 Best Local Similarity 53.7%; Pred. No. 3.4e-10;  
 Matches 198; Conservative 0; Mismatches 167; Indels 4; Gaps 3;  
 QY 69 CACCGCGGACGAGCGAGCGGCTGGTGGCGATGCGTNCCTGATGCCGCGCTGGC 128  
 DB 277 CGCCGACCGACGTCGGACACGATGAATGGCGACTCAAGATCTCCAGATCCGACGATCGC 336

QY 129 GGGATCGNCTCCTNCATCCNCGGTGATNCCCGACTTNCACAAAGCCAGGATNATGTTCA 188  
 DB 337 TAAGATTGGCTCTTCATTAGAGTCATCCCGGACTTCCCTTAACACGGAATCATGTTTCA 396  
 QY 189 GGACATCANGANGTNGTGTTCGATCCCAAGCGGTCGTTGACAAACATATACCATTTCT 248  
 DB 397 GGACATAACGACGCTTCTTCGACACATGAGGCTTTAAGGATACATATTGCTTGTTC 456  
 QY 249 CAAGCGGTACAGGACCAAGNATCACCTNCGAANTAGGATTAAGCTAGAGGNTCA 308  
 DB 457 TGATAGATACAAAGATAAAGGCATATCTGTTG-TTGCAGGTGTTCAAGCTAGAGTTTCA 515  
 QY 309 NTTTCGACACACTANNCTCTTANAANNAATTCGTCARAATGTCNCNATTCAGGAAC 368  
 DB 516 TTTTGGCCCTCTTATTCGTTG-GCTATTGGTCCCAATTTGTTCCCA-TAGGAAGC 572  
 QY 369 NNAATNAGTCCGACNCAATATGTTTNGATNATANGAATTTTNGGAATNNGAATNNT 428  
 DB 573 CCAGAAGACTACCTGGGAGGTTATTTCGGAGGAGTATTCTGTTGGAGTATGGAACAGATA 632  
 QY 429 AGATAAAAA 437  
 DB 633 CGATTGAGA 641  
 RESULT 4  
 ATAPT 729 bp mRNA linear PLN 28-APR-1992  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 A.thaliana apt mRNA for adenine phosphoribosyltransferase.  
 X58640  
 X58640.1 GI:16163  
 adenine phosphoribosyltransferase; apt gene.  
 thale cress.  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 729)  
 Moffatt,B.A.  
 Direct Submission  
 Submitted (27-MAR-1991) B.A. Moffatt, University of Waterloo, Dept  
 of Biology, Waterloo, Ontario N2L 3G1, CANADA  
 2 (bases 1 to 729)  
 Moffatt,B.A., McWhinnie,E.A., Burkhardt,W.E., Pasternak,J.J. and  
 Rothstein,S.J.  
 A complete cDNA for adenine phosphoribosyltransferase from  
 Arabidopsis thaliana  
 Plant Mol. Biol. 18 (4), 653-662 (1992)  
 92216042  
 PUBMED  
 1558943  
 Location/Qualifiers  
 1..729  
 /organism="Arabidopsis thaliana"  
 /strain="columbia"  
 /db\_xref="taxon:3702"  
 /clone\_lib="lambda gcll"  
 1..709  
 /gene="apt"  
 1..709  
 /gene="apt"  
 /evidence="experimental  
 18..569  
 /gene="apt"  
 /EC\_number="2.4.2.7"  
 /codon\_start=1  
 /product="adenine phosphoribosyltransferase"  
 /protein\_id="CAA41497.1"  
 /db\_xref="GI:16164"  
 /db\_xref="SWISS-PROT:P31166"  
 /translation="NATEDVDPRIAKTSIRVDPFKPGIMFQDITLLDTEAF  
 KDTIALVDYRDKGISVAGVEARGFPGPIALAIKAKEVPMRKKLPKGVIS  
 EYSLEYGDTIEHVGAVGERAIIDDLIATGTTAAAIRLLRERGVKIVEACVIE  
 LPELKGKELGETSLFLVLRSA"





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 04:07:43 ; Search time 2689 Seconds  
(without alignments)  
4762.081 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 440  
Sequence: 1 ggtccgcgcgcgccttc.....ggaatntagataaaaaant 440

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_da.\*
- 2: gb\_hlg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_hlg\_hum.\*
- 31: em\_hlg\_inv.\*
- 32: em\_hlg\_ther.\*
- 33: em\_hlg\_mus.\*
- 34: em\_hlg\_pln.\*
- 35: em\_hlg\_rtd.\*
- 36: em\_hlg\_mam.\*
- 37: em\_hlg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	123.6	28.1	975	8	AB012046	AB012046 Hordeum v
2	123.2	28.0	843	8	TAU22442	U22442 Triticum ae
3	88.4	20.1	1036	8	AY084300	AY084300 Arabidops
4	86.6	19.7	729	8	ATAP1	Y58640 A thaliana
5	86.6	19.7	879	8	AF325045	AF325045 Arabidops
6	86.6	19.7	887	8	AY128377	AY128377 Arabidops
7	77	17.5	847	8	AY084513	AY084513 Arabidops
8	72.4	16.5	579	8	AY133669	AY133669 Arabidops
9	69	15.7	727	8	ATAP2	X96866 A.thaliana
10	69	15.7	850	8	AY072021	AY072021 Arabidops
11	52.2	11.9	106702	8	ATF7K2	AL033545 Arabidops
12	52.2	11.9	199577	8	ATCHRIV57	AL161557 Arabidops
13	51.2	11.6	86209	8	AP004523	AP004523 Lotus jap
14	51.2	11.6	132914	2	CNS08CAA	AE031797 Oryza sat
15	50.2	11.4	10172	1	AE004187	AE004187 Vibrio ch
16	49.8	11.3	13614	1	AE006072	AE006072 Pasteurel
17	49.8	11.3	190050	1	AL646059	AL646059 Ralstonia
18	48.8	11.1	4774	1	AF109172	AF109172 Rhizobium
19	47.6	10.8	110992	8	ATF2111	AL360314 Arabidops
20	47.2	10.7	98980	2	AP004215	AF004215 Oryza sat
21	47.2	10.7	126734	8	AP003849	AP003849 Oryza sat
22	46.8	10.6	11055	1	AE009173	AE009173 Agrobacte
23	46.8	10.6	11512	1	AE008139	AE008139 Agrobacte
24	46.4	10.5	3522	1	AF421216	AF421216 Streptomy
25	46	10.5	143051	1	D90911	D90911 Synecocyst
26	45.6	10.4	137519	8	ATTP17	AL049730 Arabidops
27	45.6	10.4	196107	8	ATCHRIV34	AL161534 Arabidops
28	43.6	9.9	3761	1	PANR	X57736 P.aeruginos
29	43.6	9.9	3761	1	PSEANPRO	M98276 Pseudomonas
30	43.6	9.9	11627	1	AE004582	AE004582 Pseudomon
31	43.4	9.9	323450	1	SMES91790	AE0591790 Sinorhizo
32	43.2	9.8	10729	1	AE012338	AE012338 Xanthomon
33	43.2	9.8	179976	2	AC114702	AC114702 Rattus no
34	43	9.8	80119	2	AC119364	AC119364 Rattus no
35	42.8	9.7	2899	8	ATHAP1A	LI9637 Arabidops
36	42.8	9.7	99690	8	AC004557	AC004557 Genomic s
37	42.6	9.7	348077	1	AP003000	AP003000 Mesorhizo
38	42.2	9.6	851	1	ECOAPT	M14040 E.coli apl
39	42.2	9.6	6820	1	ECOAPTADK	M38777 E.coli sequ
40	42.2	9.6	10103	1	AE000153	AE000153 Escherich
41	42.2	9.6	139818	1	FCU82664	UB2664 Escherichia
42	42.2	9.6	192657	1	AP005377	AP005377 Thermosyn
43	42	9.5	3322	8	RICFUJI	D50602 Rice mRNA f
44	42	9.5	15248	8	AB012915	AB012915 Oryza sat
45	42	9.5	348550	1	AP003596	AP003596 Nostoc sp

ALIGNMENTS

RESULT 1  
AB012046

LOCUS

DEFINITION

AB012046 Hordeum vulgare HvAPRT1 mRNA for Adenine phosphoribosyltransferase,  
complete cds.

ACCESSION

AB012046.1

VERSION

HvAPRT1: Adenine phosphoribosyltransferase.

KEYWORDS

Hordeum vulgare (variety: Ehmebadaka no.1) root cDNA to mRNA.

SOURCE

Hordeum vulgare subsp. vulgare

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooidae; Triticeae; Hordeum.

REFERENCE

1 (sites)

AUTHORS

Itai,R., Suzuki,K., Yamaguchi,H., Nakanishi,H., Nishizawa,N.K.,

QY 90 GCGGTGTGCGGATG 105  
|||||  
Db 1149 GCGGTGTGCGGATG 1164

Search completed: November 30, 2002, 04:02:23  
Job time : 63 secs

```
US-09-981-353-109
Query Match      3.6%; Score 16; DB 9; Length 1870;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 GCGAGCGCGTGTGCG 101
Db 736 GCGAGCGCGTGTGCG 721

RESULT 13
US-09-815-242-7695
; Sequence 7695, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7695
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1998)
US-09-815-242-7695
Query Match      3.6%; Score 16; DB 10; Length 1998;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGGCGCGACTTCGCC 23
Db 996 GCGGCGCGACTTCGCC 1011

RESULT 14
US-09-938-842A-4602/c
; Sequence 4602, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
```

```
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938.842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4602
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4602
Query Match      3.6%; Score 16; DB 9; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 239 ACCATTTCACGCG 254
Db 1871 ACCATTTCACGCG 1856

RESULT 15
US-09-815-242-7991
; Sequence 7991, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7991
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2208)
US-09-815-242-7991
Query Match      3.6%; Score 16; DB 10; Length 2208;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



FEATURES	Source	Location/Qualifiers
1..847	1..847	
Source	Arabidopsis thaliana	
db_xref="taxon:3702"		
clone="11009"		
134..705		
cds		
codon_start=1		
product="adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein"		
protein_id="AA061081.1"		
db_xref="GI:21536749"		
translation="MSGNEEDPRHIGIKIRVVPPFKKIMFQDITVLLDPKA FKDTIDLFERYRDNKISVAGIEARGFLGPPALAIAGKFLPLRKPRLPGETIFE EYELGNDRLMHIGAVAGRSLSVDDLIATGTLCAAINLLRVAEWEACAVI ELPKGRQRKLGKPLVLYVEYR"		
BASE COUNT	245 a	150 c 199 g 253 t
ORIGIN		
Query Match	17.5%	Score 77; DB 8; Length 847;
Best Local Similarity	54.1%	Pred. No. 1.5e-07;
Matches	160; Conservative	0; Mismatches 133; Indels 3; Gaps 2;
QY	115	GATCGCGCTGGCGGNGATCGTCTTCATCCGNGTATCCGACTTCCAAAGCCA 174
DB	178	GATCCTCGTATCCATGAATCAAACTAAGATCCGTCGTTCAGATTTTCCCAAGAAA 237
QY	175	GGGATNATGTTTCAGGACATCANGANGTGTTCGATCCCAAGGCGTCCGTGACAAAC 234
DB	238	GGAATATGTTTCAAGACATAACACAGCTGTGTGGATCCGAAAGCCCTTCAAGACAGA 297
QY	235	ATATACCATTTTTCAGCGGTACAGGACCAAGGNATCACCTGTGGAATAGGAGTTAA 294
DB	298	ATTGATCTGTTTGGAGAGGTACAGACAGAACATCTCAGTGG-TTCAGGAATAGA 356
QY	295	ACGTAGAGGNTCANTTTCCGACACACTNNTCTTANANNAATGTTCCAAATNGGTG 354
DB	357	GGCTGCTGTTCTATTCGTCACCGA--TCGCGCTAGCCATGGACCAAAATTTGTT 414
QY	355	NCNATTGAGGAGCANNATNAGTCCAGCNAATGATTNANGAANTAGAAAT 410
DB	415	CTCTCCGCAACCCAGAACTACTCGTGGTAACCAATTTTGGAGTAATACGRTT 470
RESULT 8		
AY133689		
LOCUS	579 bp	mrna linear PLN 07-AUG-2002
DEFINITION	Arabidopsis thaliana clone C103141 (B) putative adenine phosphoribosyltransferase (At4g12440) mRNA, complete cds.	
ACCESSION	AY133689	
VERSION	FLI_CDNA.1	GI:22136607
KEYWORDS	Arabidopsis thaliana	
SOURCE	Arabidopsis thaliana	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 579)	
REFERENCE	Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R., and Theologis, A.	
AUTHORS	Arabidopsis Open Reading Frame (ORF) Clones	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 579)	
REFERENCE	Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R., and Theologis, A.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-JUL-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA	

FEATURES	Source	Location/Qualifiers
1..579	1..579	
Source	Arabidopsis thaliana	
db_xref="taxon:3702"		
clone="103141 (B)"		
note="This clone is in puni 51."		
scotype: Columbia		
1..579		
gene		
1..549		
cds		
codon_start=1		
product="putative adenine phosphoribosyltransferase"		
protein_id="AA091623.1"		
db_xref="GI:22136608"		
translation="MSENEVKDPDRIDIGIKIRVVPPFKKIMFQDITVLLDPKAF KDTIDLFERYRDNKISVAGIEARGFLGPPALAIAGKFLPLRKPRLPGETIFE EYELGSDLEHNEAVDSGDRALVVDLIATGTLCAAMNLLKRVGAIEVCACVIE IPELKGRELRKGLPLYLYVEYR"		
BASE COUNT	163 a	101 c 150 g 165 t
ORIGIN		
Query Match	16.5%	Score 72.4; DB 8; Length 579;
Best Local Similarity	52.6%	Pred. No. 1.6e-06;
Matches	159; Conservative	0; Mismatches 140; Indels 3; Gaps 2;
QY	115	GATCGCGCTGGCGGNGATCGTCTTCATCCGNGTATCCGACTTCCAAAGCCA 174
DB	22	GATCCTCGTATCGATGGTATCAAACTAGATCCGTCGTTCAGATTTTCCCAAGAAA 81
QY	175	GGGATNATGTTTCAGGACATCANGANGTGTTCGATCCCAAGGCGTCCGTGACAAAC 234
DB	82	GGTATATGTTTCAAGACATAACACAGCTGTGTAGATCCTTAAGCCTTAAAGACACC 141
QY	235	ATATACCATTTTTCAGCGGTACAGGACCAAGGNATCACCTGTGGAATAGGAGTTAA 294
DB	142	ATTGATCTGTTTGGAGAGGTATCGAGACATGAACATCTCGGTGG-TTCAGGTATAGA 200
QY	295	ACGTAGAGGNTCANTTTCCGACCAACTANNTCTTANANNAATTTGGTCAAAATNGGTG 354
DB	201	GGCTGCGGTTTCATATTCGGTTCCACCA--TCGCATTAGCCATCGGAGCAAAATTTGT 258
QY	355	NCNATTGAGGAGCANNATNAGTCCAGCNAATGATTNANGAANTAGAAATTTTNG 414
DB	259	CTCTCTCTGTAACCAAGAAATTTCCGCGCCCAATAATATTTTGAAGAGTATGAGTTGGAG 318
QY	415	GA 416
DB	319	TA 320
RESULT 9		
ATAPT2		
LOCUS	727 bp	mrna linear PLN 20-NOV-1996
DEFINITION	A.thaliana Atapt2 mRNA for adenine phosphoribosyltransferase.	
ACCESSION	X96866.1	GI:11402893
VERSION	adenine phosphoribosyltransferase; Atapt2 gene.	
KEYWORDS	Thale cress.	
SOURCE	Arabidopsis thaliana	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 727)	
REFERENCE	Schnorr, K.M.	
AUTHORS		

Query Match 15.7%; Score 69; DB 8; Length 850;  
Best Local Similarity 50.2%; Pred. No. 1e-05;





exon RVRTGKAKAMEKYLKVKKSG\*  
 complement(13513). .13618)  
 /gene="AT4g22420"  
 /number=1  
 intron complement(13619). .13700)  
 /gene="AT4g22420"  
 /number=1  
 exon complement(13701). .14033)  
 /gene="AT4g22420"  
 /number=2

Query Match 11.9%; Score 52.2; DB 8; Length 106702;  
 Best Local Similarity 63.7%; Pred.No. 0.18;  
 Matches 72; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 168 AAGCCAGGATNATGTTTCAGGACATCANGANGTNGTTCGATCCCAAGCGNCCG 227  
 DB 72738 AATTCAGGAATAATCTTCAAGACATACAACACGTGTTCTGATCCGAAAGCCTCAA 72679  
 QY 228 TGACACATATACCATTTGTTCAGCGGTACAGGACCAAGGNATCACCTGG 280  
 DB 72678 AGACACATTCATCTGTTGTCGAGAGCTACAGACACAGCAATCTCAGTGG 72626

RESULT 12  
 ATCHRIV57/c

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
ATCHRIV57	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57.	AL161557	AL161557.2	GI:7269071	Arabidopsis thaliana.	Arabidopsis thaliana.
LOCUS	Arabidopsis thaliana	ATCHRIV57	199577 bp	DNA	linear	PLN 16-MAR-2000
DEFINITION	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57.	AL161557				
ACCESSION	AL161557					
VERSION	AL161557.2					
KEYWORDS						
SOURCE	Arabidopsis thaliana.					
ORGANISM	Arabidopsis thaliana					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.					
AUTHORS	1. (bases 48809 to 64829) Robben,J., Grymonprez,B., Volckaert,G., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished					
JOURNAL	Unpublished					
REFERENCE	2. (bases 64578 to 155510) Wedler,H., Wambutt,R., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished					
AUTHORS	3. (bases 141638 to 141797) Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished					
JOURNAL	4. (bases 143670 to 199577) Hilbert,H., Braun,M., Holzer,E., Brandt,A., Duesterhoeft,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished					
REFERENCE	5. (bases 1 to 199577) EU Arabidopsis sequencing, project.					
AUTHORS	Direct Submission					
TITLE	Submitted (10-MAR-2000) MIPS, at the Max-planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG. E-mail: lemcke@mps-biochem.mpg.de, mayer@mps-biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk					
JOURNAL	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ this fragment has an overlap with ATCHRIV56 at the 5' end and an overlap with ATCHRIV58 at the 3' end.					
COMMENT	Location/Qualifiers 1. .199577 /organism="Arabidopsis thaliana" /variety="Columbia" /db_xref="taxon:3702" /chromosome="4" 6674. .9057 /gene="AT4G22360"					
FEATURES	source					
gene						

```
gene      complement(join(6674..6882,7268..7339,7507..7575,
7667..7775,7863..7978,8361..8454,8588..8777,8909..9057))
/ gene="AT4g22260"
CDS      complement(join(6674..6882,7268..7339,7507..7575,
7667..7775,7863..7978,8361..8454,8588..8777,8909..9057))
/ gene="AT4g22260"
/ note="similarity to alternative oxidase, Mangifera
indica, PIR2:845035
contains EST gb:742793, AI994896.1, AI997645.1, R30022,
AA395166"
/ codon_start=1
/ product="putative protein"
/ protein_id="CAB79181.1"
/ db_xref="GI:7269073"
/ translation="MAISGISGCLTISRPLVLRBSAAVSYSSSHLLHLPLSS
RLLLNHRVATLIQDDEKVVVEESFKAETSTGTETPLEPNHSSSTSAETWII
KLEGVNVEFTDSVKILIDLYIKDRTYARFVLETTIARVPIAFMSVLHAYENFGWR
RADLYKVHFAESNMHLLIMEELGNSWFDPLAQHIAITFTFMVFLIILSPRM
AYHSECVSHAYETDGFKAEGELKNMFPADIAVKYTGDDLYLFENLIDFVNI
RDDAECKTMRACQTLGSLRSPHSITLEDODTEESGCVVPEAHCEGIVDCLKRSIT
S"
exon      complement(6674..6882)
/ gene="AT4g22260"
/ number=1
intron    complement(6883..7267)
/ gene="AT4g22260"
exon      complement(7268..7339)
/ gene="AT4g22260"
/ number=2
intron    complement(7340..7506)
/ gene="AT4g22260"
/ number=3
exon      complement(7507..7575)
/ gene="AT4g22260"
/ number=4
intron    complement(7576..7666)
/ gene="AT4g22260"
/ number=5
exon      complement(7667..7775)
/ gene="AT4g22260"
/ number=6
intron    complement(7776..7862)
/ gene="AT4g22260"
/ number=7
exon      complement(7863..7978)
/ gene="AT4g22260"
/ number=8
intron    complement(7979..8360)
/ gene="AT4g22260"
/ number=9
exon      complement(8361..8454)
/ gene="AT4g22260"
/ number=10
intron    complement(8455..8587)
/ gene="AT4g22260"
/ number=11
exon      complement(8588..8777)
/ gene="AT4g22260"
/ number=12
intron    complement(8778..8908)
/ gene="AT4g22260"
/ number=13
exon      complement(8909..9057)
/ gene="AT4g22260"
/ number=14
gene      join(10103..10244,10395..10516,11327..11779,11868..12174,
12254..12393)
CDS      join(10103..10244,10395..10516,11327..11779,11868..12174,
12254..12393)
/ note="contains EST gb:AI997575.1"
/ codon_start=1
```

```
/ product="hypothetical protein"
/ protein_id="CAB79182.1"
/ db_xref="GI:7269073"
/ translation="MATNGSSSHELLPETPSALINKOQEPFASRFTFMSLVLWFDQ
SNGSISFSLSSWKKKGRRELFLDKLWVSKVRIEYEAETORSILKRLMIFVLPSL
TLEATIRWIIYSIGFNLPYIINPLSHVACTLOISSLVYNSFTILICILYKITCH
LOTLRDDPFCFASLITDVRSLGELHOKIRRNLRVSHRFRRTILSLIVATQFM
ALUTTRASVAVNIYEGVLAELCSLSLVFICLASAKITHKAQSVTSLAAKNVC
ATVDSFDHLDGTPGSLTIESQVSURGNAIETSDDEGGDDDLNTKIIPIYANTIS
YORQALVYILENNKAGITVYGLVDRSWLNTIFGIELALLWLLKLTIGILA"
10103..10244
/ gene="AT4g22270"
/ number=1
intron    10245..10394
/ gene="AT4g22270"
/ number=1
exon      10395..10516
/ gene="AT4g22270"
/ number=2
intron    10517..11326
/ gene="AT4g22270"
/ number=3
tRNA      11168..11253
/ gene="AT4g22270"
/ product="tRNA-Tyr"
/ note="codon recognized: GUA"
11327..11779
/ gene="AT4g22270"
/ number=3
intron    11780..11867
/ gene="AT4g22270"
/ number=3
exon      11868..12174
/ gene="AT4g22270"
/ number=4
intron    12175..12253
/ gene="AT4g22270"
/ number=4
exon      12254..12393
/ gene="AT4g22270"
/ number=5
gene      12761..15111
/ gene="AT4g22280"
complement(join(12761..13015,13081..13227,13379..14157,
14209..14314,14995..15111))
/ gene="AT4g22280"
complement(join(12761..13015,13081..13227,13379..14157,
14209..14314,14995..15111))
/ gene="AT4g22280"
/ note="similarity to hypothetical protein, chr.4,
Arabidopsis thaliana, PATCHX.G2392763
contains EST gb:AI998861.1, AI993240.1"
/ codon_start=1
/ product="putative protein"
/ protein_id="CAB79183.1"
/ db_xref="GI:7289074"
/ translation="MEKDVMTDTCVGNRPATIVNGLNISHOCMTSLKVCVIF
FCVWDAGDLFLRLITPERFIRIWMQDRINEATSYLSMRWRYLFAFPNKLDDGE
VGGDSFIDFVRVIVTGNFPIRRISIKRMSIDTGHVTHMVDVLEHGVSYLDIDI
ISEDIGFVLEIFTCKLVELKARFAMVPDYSLPSLTKTLFLUSSIFCNKDCCP
LGRLLSAPVLEELITIGGCWOHIEFCRTVSSSTLKLITTSFHYEWGITDTPSL
AYLEYSDLVPRHFFVNLESIAEKALDICSNSPTNLKGRNVLEVLSGGYTSQ
ILYDFRAIPVLKSLFRISIKSNHYIWNLLPILLEKSPKLETIVIKGPLSADRYE
REYGLSCPVKVLEITYGKYEELEQMEHFLKPLCLPLVKVRASAINDKESRITKD
LLMWPRSSNCNIKFC"
complement(12761..13015)
/ gene="AT4g22280"
/ number=1
intron    complement(13016..13080)
/ gene="AT4g22280"
/ number=1
exon      complement(13081..13227)
/ gene="AT4g22280"
```



```

source
1. .132914
/organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="12"
/clone="OSJNBa0010M16"
/clone_1lb="OSJNBa"

BASE COUNT      38909 a 26633 c 28047 g 38625 t      700 others
ORIGIN

Query Match      11.6%; Score 51.2; DB 2; Length 132914;
Best Local Similarity 57.6%; Pred. No. 0.31;
Matches 80; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 174 AGGATNATGTTTCAGACATCANGANTGNTGTCGATCCCAAGCGGTCGTCGACAA 233
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 108630 AGGATCTGCTTTCAGGATGTCACGGTATATTCACAACCGGATTCGTCGATGC 108571

QY 234 CATATACCATTTTGTCAAGCGGTACAAGGACCAAGNATCACCTGCAAGTAGGATTA 293
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 108570 CATCGGCTGTTTCGTCGAGAGGTACAAGGCAAGGGGTCTCTTCTAGCTGTAATTA 108511
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 294 AAGCTAGAGGNTTCATTTT 312
      |||||
Db 108510 ATCTGAACATATGATTT 108492
      |||||

RESULT 15
LOCUS      AE004187
DEFINITION Vibrio cholerae chromosome 1, section 95 of 251 of the complete
            chromosome
ACCESSION  AE004187 AE003852
VERSION    AE004187.1 GI:9655516
KEYWORDS
SOURCE     Vibrio cholerae.
ORGANISM   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
REFERENCE  1 (bases 1 to 10172)
            Heidelberg, J.P., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,
            Dodson, R.J., Haft, D.H., Hickley, E.K., Peterson, J.D., Umayam, L.,
            Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.,
            Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragol, I.,
            Sellers, P., McDonald, L., Utterback, T., Fleischmann, R.D.,
            Nierman, W.C. and White, O.
            DNA sequence of both chromosomes of the cholera pathogen Vibrio
            cholerae
            Nature 406 (6795), 477-483 (2000)
            20406833
            10952301
            2 (bases 1 to 10172)
            Heidelberg, J.P., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,
            Dodson, R.J., Haft, D.H., Hickley, E.K., Peterson, J.D., Umayam, L.,
            Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.,
            Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragol, I.,
            Sellers, P., McDonald, L., Utterback, T., Fleischmann, R.D.,
            Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R.,
            Mekalanos, J.J., Venter, J.C. and Fraser, C.M.
            Direct Submission
            Submitted (14-JUN-2000) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
FEATURES
source
1. .10172
/organism="Vibrio cholerae"
/strain="N16961"
/serotype="O1"
/db_xref="taxon:666"
/chromosome="1"
/note="biotype: El Tor"
116. .247
/gene="VC1051"
116. .247

gene
CDS

/feature="VC1051"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAF94210.1"
/db_xref="GI:9655517"
/translation="MANQEKPEPNYYELGVAVLLIPLTLPATLTWIRVFNQYAGF"
247. .645
/gene="VC1052"
247. .645
/gene="VC1052"
247. .645
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAF94211.1"
/db_xref="GI:9655518"
/translation="MRSSLPRLFTVIGTISLCILGILFPLPTPTPFIILLSSACFL
RSSPFRWLNOHATFGPMIONQOHCAYSKAVKRATLIVLSFAPSMVWPMILK
VALFTWLVLITWIRLPHLTHLVANQENH"
777. .1322
/gene="VC1053"
777. .1322
/gene="VC1053"
777. .1322
/note="similar to GB:M14040 SP:P07672 GB:X04487 PID:145294
PID:145296; identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
/product="adenine phosphoribosyltransferase"
/protein_id="AAF94212.1"
/db_xref="GI:9655519"
/translation="MTTSLIKSSIKIPDKGILFEDVTSLLSDAQAQNTIO
LLVYKDMKFTVGTGARGELFCAPLALGELGCVFVPRKCKLPCTVQAQSYLEY
GDTLELHVDALEPKDKLVVDLLATGTTIATKLRQGGVEHAFVNLPEIG
GSKRLEGLGVYSICEFEGH"
1341. .3419
/gene="VC1054"
1341. .3419
/note="similar to GB:N38777 SP:P06710 GB:X04275 GB:X04487
PID:145297; identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
/product="DNA polymerase III, subunits gamma and tau"
/protein_id="AAF94213.1"
/db_xref="GI:9655520"
/translation="MSYIALARKWPRFSEVVGSHVLTALENALQNRHHAYLFS
GTGVRKTTIGRLFAGKNCETGITATPCGCATCQEIQDGRVLDLEIDRAKTRQE
DPTRELLNVOYKPARGRKXVLIIDEVHLSRHSFNAKLTLEPPYKFLATDQ
KLTTLISRLCQFLHUKPISVENIQQDKVYHABQISDSKALNLAHAADGSRDLQ
SLTDALALGVVSDIVAHMLGTDIDHSLLHQAISLQTPVAMOCITETLAQNGV
EDWGLJLQSTQHRILAMYPATLIDKSLPNSRISLAKTLAPDQVLYYQIALKG
RQDPLSPRTARIGTETMLRMHAPRSHVSLASIVPNTAVTPIATPQSOHAAA
PQPVQAQNSQSASQAMPHPVAPPMMAQPVESAVPTQREASHSINAPASVYT
NFTDSQASMPALAGRLHRLKSRQVQNGKADGKSDATSPASALERIQAQGVV
QVSPRNDDELEPEEYIQRPMQPIEVAKVSEVPTQLKALBREKTPAQAKLIE
EAVADWASVALVRLTAKMVEQLANSAFVQGDQISLTLRPSHAHUNKEAQOOLE
QALNHLVGEACSLNITVGOGETPLELRERLYQOKLTLSALHSLQTDPNVQFIERRNA
QDSDSVRPI"
3457. .3819
/gene="VC1055"
3457. .3819
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAF94214.1"
/db_xref="GI:9655521"
/translation="MKHSTITREIKMFGKGMGNLMKQAQOQMKOERKQLEIANMEV
TGSGAGLVKVTGTVTGSRRVNRINDELMEDDKMLEDLIAAFNDAARITEETQERK
MASITGGQMLPCKMKMPF"

```

```

3834. 4436
/ gene="VC1056"
/ CDS
/ note="similar to GB:M38777 SP:P12727 GB:X15761 PID:145299
PID:42697; identified by sequence similarity; putative"
/ codon_start=1
/ transl_table=11
/ product="recombination protein Recr"
/ protein_id="AAF94215.1"
/ db_xref="GI:9655523"
/ translation="MRTSHMLHEALRCLFVGPKSAQRMAFHLLQDRKGGSLQLA
EALSQAMVIGICQCRFTTEQDVCHICSNPKRKGOLCVVESPADIALEATGQFS
GRYELVGLSLDIDGPSIDIGDITLDRLOGLDISVILATNPVEGEATQYIAEL
CREHQVTASRIAGHPVVGLELVDGTTLSHLLGRHLF"
/ complement(4546. .4797)
/ gene="VC1057"
/ CDS
/ complement(4546. .4797)
/ gene="VC1057"
/ note="similar to GB:U73004 SP:P97430 PID:1763263
PID:1945383 PID:1945451; identified by sequence
similarity; putative"
/ codon_start=1
/ transl_table=11
/ product="proteinase inhibitor, putative"
/ protein_id="AAF94216.1"
/ db_xref="GI:9655523"
/ translation="MMDCRLGCGACCTAPSISSPIPGMNGKRPAGVRCVOLNEDNLCO
LFGRPCKVCHDFKACPVVCGKTNQALANLTELRL"
/ 4932. 5369
/ gene="VC1058"
/ CDS
/ 4932. 5369
/ gene="VC1058"
/ note="identified by Glimmer2; putative"
/ codon_start=1
/ transl_table=11
/ product="conserved hypothetical protein"
/ protein_id="AAF94217.1"
/ db_xref="GI:9655524"
/ translation="MSIPFQWQSTLDQMTAEWESLDCGCGCKLHKLMDEDDTEIYY
TNVACSWNSDTCSCDFRFSGGECLKTRKIEEFNWLPTCAIRLNGNQTLF
EWHPLLRGSKDAHANDESVRGKIVYEDVIDWEDHIVLMKRD"
/ complement(5463. .6206)
/ gene="VC1059"
/ CDS
/ complement(5463. .6206)
/ gene="VC1059"
/ note="similar to SP:P31808 GB:U17433 PID:603171 GB:U00096
PID:1742066; identified by sequence similarity; putative"
/ codon_start=1
/ transl_table=11
/ product="oxidoreductase, short-chain
dehydrogenase/reductase family"
/ protein_id="AAF94218.1"
/ db_xref="GI:9655525"
/ translation="MNYSVSTDALEKEKVLVTGAGDIGKQAAISFAAAGATVILLGR
TVKLEQYDAEAAQYPAIVPLDMKATKQNYLDMVDTEDOFGRLOQVLHNASL
LGVLSPDQIGDSDPEVMQVNVKAQFLMTQALLPLLRKSADARIVFTTSTVGHIGRA
FWATYALSKFATEGMQILADELSESTIRVNAINPGGTRTAMRAKAYPAEDADKLKTP
LDIMPLYLYLMAPEGREVHQCIDAQPKK"
/ 6356. 7426
/ gene="VC1060"
/ CDS
/ 6356. 7426
/ gene="VC1060"
/ note="similar to GB:M73320 SP:P24213 PID:290470 GB:U00096
PID:1742067; identified by sequence similarity; putative"
/ codon_start=1
/ transl_table=11
/ product="schB protein, peptidase U7 family"
/ protein_id="AAF94219.1"
/ db_xref="GI:9655526"
/ translation="MSHLELLDYCLFLAKITVVVALVAVLVIVKSLGCRSGKMGKE
LEITDTEOKETVEPEALVHDEPAELKAROKADKKKEKREKSLQAKKEGEL
ESKADPHLVLDLPHSDIAKEVSAASREVSAILAVQAGDEVLLRLLETGGGWHGIGL

```

```

ASSOLDRLKAAGLPTTANDKVAASGGTMMACIADKIIVSAPFAIVGSIGVVAQLPNFH
KLLKNDIEFQTAGETKRTLTMEGENTDKAREKFKQELDEHQLKDFIREHRPAL
DLKQVATGEHFGTQAKAUGLVDIEIQTSDDLIVAACKSKTVLLRLRYTKRKLADKLAG
VAGDAADNVLLRLLSRGORPLV"
/ complement(7551. .8618)
/ gene="VC1061"
/ CDS
/ complement(7551. .8618)
/ gene="VC1061"
/ note="similar to GB:ALL123456; identified by sequence
similarity; putative"
/ codon_start=1

Query Match 11.4%; Score 50.2; DB 1; Length 10172;
Best Local Similarity 55.0%; Pred. No. 0.35;
Matches 82; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 132 GATCGNCTCTNCACTCCNGGTNATNCCGACTTNCCAAAGCCAGGATNATGTTTCAGGA 191
||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 800 GATCAAAATCCAGCATCAAAAAGTATTCCTGACTACCCGAAAAAAGGCATTCGTTTCGTA 859
QY 192 CATCANGANGNTGNTTTCGATCCCAAGCGGNTCCGTGACACATATACCATTTGTCAA 251
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 860 TGTGACCACTTGTCTGGAAGATGCCAAGCCTACCAAGCGCATTCACTTCGTGTA 919
QY 252 GCGGTACAAAGGACCAAGGNNATCACCNTGS 280
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 920 AAAGTACAAAGACATGGGTTTTTACCAGG 948

Search completed: November 30, 2002, 05:56:47
Job time : 2954 secs

```





US-08-447-010-1

Query Match 19.7%; Score 86.6; DB 1; Length 729;  
Best Local Similarity 55.7%; Pred. No. 1,5e-15;  
Matches 180; Conservative 0; Mismatches 139; Indels 4; Gaps 3;

QY 115 GATGGCGCCTTGGCGGNGATCGNCTCTNCATCCGNGTATNCCGACATTCACCAAGCCA 174  
DB 39 GATCCCAAGATCCGCTAAGATTCGCTTCCTATAGAGTATCCCGACATCCCTTAACCA 98  
QY 175 GGAATGATGTTTCAGGACATCANGANGNTGNTGTCGATCCCAAGCGCTCCGTGACAC 234  
DB 99 GGAATCATGTTTCAGGACATACACGCGCTCTCTCGACACTGAGCGCTTTAAGGATACT 158  
QY 235 ATATACCATTTTGTCAAGCGGTACAGGACCAAGNATCACCTTCTTANAANAATTTGGTCAAAAATNGTG 294  
DB 159 ATTGCTTTGTTGTATAGATACAAAGATTAAGCATATCTCTTG-TTGCAGAGGTGA 217  
QY 295 AGCTAGAGGGTTCANTTTCCGGAACAACATNNTCTTANAANAATTTGGTCAAAAATNGTG 354  
DB 218 AGCTAGAGGTTTCATTTTGGCCCTCTTATGCGTTG--GCTATTGGTCCAAATTTGTT 275  
QY 355 NCNATGAGGAAGCNAATNAGNTGCCANGCNAATGATTTTNGACATANGAATTTTNG 414  
DB 276 CCACTGAGGAAGCCCAAGAGCTACCTGGGAAGGTATTTTCGAGGAGTATTCGTTGA 334  
QY 415 GAATNNGCAATNTAGATAAAAA 437  
DB 335 GTATGGAACAGATACGATTGAGA 357

## RESULT 2

US-09-103-840A-2/C  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 8.4%; Score 36.8; DB 4; Length 4403765;  
Best Local Similarity 45.4%; Pred. No. 9.2;  
Matches 98; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 14 CGACTTCGCTTTTTCGTCGCCGCTGACGCTCCGCTCCNNTGAGCGTGCCTGACCG 73  
DB 3716700 CCACCTTCGCGTCCAGGAAGCGCGGATCGCGCATCGCTTCGGGCAACTCGGGTGCCA 3716641  
QY 74 GCGGACGCGAGGCGGCGGTGGTGGCGATGGCTNGCTGCTGATCGCGCTTGGCGGNGA 133  
DB 3716540 ACGTGACCATTCGCGGACGCGCGCTGCGGCGGAGCACCACCTCGATCTCGCGGAT 3716591  
QY 134 TCNGTCTTCNATCCNGTTCATNCCGACTTCNCAAGCCAGGGATNATGTTTCAGACA 193  
DB 3716580 CCGGGGACCGCATCCCGGGGTG76GTGCTGCCGTCCCGCACCGCGCTGGGTAGCCAGCGCC 3716521

QY 194 TCANGANGNTGTTTGGATCCCAAGCGGNTCCGTG 229  
DB 3716520 CCTCCAGATGATGCCCGGACGACGCGCTCCCGAG 3716485

## RESULT 3

US-09-103-840A-1/C  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37RV  
US-09-103-840A-1

Query Match 8.0%; Score 35.2; DB 4; Length 4411529;  
Best Local Similarity 45.4%; Pred. No. 23;  
Matches 98; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 14 CGACTTCGCTTTTTCGTCGCCGCTGACGCTCCGCTCCNNTGAGCGTGCCTGACCG 73  
DB 3719140 CCACCTTCGCGTCCAGGAAGCGCGGATCGCGCATCGCTTCGGGCAACTCGGGTGCCA 3719081  
QY 74 GCGGACGCGAGGCGGCGGTGGTGGCGATGGCTNGCTGCTGATCGCGCTTGGCGGNGA 133  
DB 3719080 ACGTGACCATTCGCGGCGCGCTGCGGCGGAGCACCACCTCGATCTCGCGGAT 3719021  
QY 134 TCNGTCTTCNATCCNGTTCATNCCGACTTCNCAAGCCAGGGATNATGTTTCAGACA 193  
DB 3719020 CCGGGGACCGCATCCCGGGGTG76GTGCTGCCGTCCCGCACCGCGCTGGGTAGCCAGCGCC 3718961  
QY 194 TCANGANGNTGTTTGGATCCCAAGCGGNTCCGTG 229  
DB 3718960 CCTCCAGATGATGCCCGGACGCGCGCTCCCGAG 3718925

## RESULT 4

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g



US-09-103-840A-2

Query Match 8.0%; Score 35; DB 4; Length 4403765;  
Best Local Similarity 47.1%; Pred. No. 26;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 43 GTCCGGGTCCTCCTGCGGTGCGGTCAACCGGGCAGCGAGGGGAGGGGTTGGG 102  
DB 591548 GTGGCGGAGCGGATGCCCGATCGCGCAACTACCTGGCGACACCTATTCGGTGTGGTG 591607  
QY 103 ATGGCGTNCGTGATCGCGGTGGCGGNGATCGCTCCTNCATCCNGGTTNATNCCCGAC 162  
DB 591608 AGCTGGCGGCGGAGCGGTGGAGACGCGACGTTCGTGCTGCGGCGTCAAAACAGCC 591667  
QY 163 TTNCAAAGCCAGGATNATGTTTCAGGACATCANGANTGNTGTTCTGA 212  
DB 591668 GACGTCGAGCGGTGATCGCGATCTGCGAAGCGGACTGCGGCGGCGGA 591717

RESULT 5

US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 8.0%; Score 35; DB 4; Length 4411529;  
Best Local Similarity 47.1%; Pred. No. 26;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 43 GTCCGGGTCCTCCTGCGGTGCGGTCAACCGGGCAGCGAGGGGAGGGGTTGGG 102  
DB 590186 GTGGCGGAGCGGATGCCCGATCGCGCAACTACCTGGCGACACCTATTCGGTGTGGTG 590245  
QY 103 ATGGCGTNCGTGATCGCGGTGGCGGNGATCGCTCCTNCATCCNGGTTNATNCCCGAC 162  
DB 590246 AGCTGGCGGCGGAGCGGTGGAGACGCGACGTTCGTGCTGCGGCGTCAAAACAGCC 590305  
QY 163 TTNCAAAGCCAGGATNATGTTTCAGGACATCANGANTGNTGTTCTGA 212  
DB 590306 GACGTCGAGCGGTGATCGCGATCTGCGAAGCGGACTGCGGCGGCGGA 590355

RESULT 6

US-08-525-864A-1/c  
; Sequence 1, Application US/08525864A  
; Patent No. 5912326  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Han  
; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/525,864A  
FILING DATE: 8-SEP-1995  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Kara, Catherine J.  
REGISTRATION NUMBER: 41,106  
REFERENCE/DOCKET NUMBER: HUI-017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3441 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 180..2441  
US-08-525-864A-1

Query Match 7.9%; Score 34.8; DB 2; Length 3441;  
Best Local Similarity 60.7%; Pred. No. 1.7;  
Matches 54; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 36 GTCCAGCGTCGCGGCTCCNTGACGTGCGCTACCGCGGCGGAGCGGAGCGGCGGT 95  
DB 2122 CCCCAGCGCGCGCGCGCGCGCGCGCGCTCTCGCGGAGCGCGCGCTGCGGCGGCGG 2063  
QY 96 GTGGCGGATGCGGTTCGCTGATGCGCGCT 124  
DB 2062 GTGGCGGCGGCGCGCACTCTCTGCGTGT 2034

RESULT 7

US-08-519-777-30  
; Sequence 30, Application US/08519777  
; Patent No. 5735307  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILLERANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/519,777  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197

```
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-519-777-30

Query Match 7.8%; Score 34.4; DB 1; Length 419;
Best Local Similarity 47.0%; Pred. No. 0.87;
Matches 86; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1 CGTCCGGCGCGGCGGCTTGGCTTTTGGTCCCGCGCTCAGCGTCCGCGGCTCCNNTGAGC 60
DB 105 CGCGCGCGCGCGCGGCGGCTTGGCTTTGGTCCCGCGAGCTCGAGGTGCGCGTGAGC 164
QY 61 GTCCGCGTACCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 165 GAGCTGGGCGTGGCTACACGTCGATGAGACCGTGTCTTCCGCTACTCCGCGAGCGCG 224
QY 121 CGCTTGGCGGCGGATCGNCTCTTCATCCGCGGATNCCCGAGCTTNCAGAGCGGATN 180
DB 225 TCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 284
QY 181 ATG 183
DB 285 GTG 287

RESULT 8
US-08-742-035-30
; Sequence 30, Application US/08742035
; Patent No. 5747655
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEUTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,035
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-777-019-30

; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-742-035-30

Query Match 7.8%; Score 34.4; DB 1; Length 419;
Best Local Similarity 47.0%; Pred. No. 0.87;
Matches 86; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1 CGTCCGGCGCGGCGGCTTGGCTTTTGGTCCCGCGCTCAGCGTCCGCGGCTCCNNTGAGC 60
DB 105 CGCGCGCGCGCGCGGCGGCTTGGCTTTGGTCCCGAGCTCGAGGTGCGCGTGAGC 164
QY 61 GTCCGCGTACCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 165 GAGCTGGGCGTGGCTACACGTCGATGAGACCGTGTCTTCCGCTACTCCGCGAGCGCG 224
QY 121 CGCTTGGCGGCGGATCGNCTCTTCATCCGCGGATNCCCGAGCTTNCAGAGCGGATN 180
DB 225 TCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 284
QY 181 ATG 183
DB 285 GTG 287

RESULT 9
US-08-777-019-30
; Sequence 30, Application US/08777019
; Patent No. 5817622
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEUTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,019
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-777-019-30
```

```
Query Match          7.8%; Score 34.4; DB 1; Length 419;
Best Local Similarity 47.0%; Pred. No. 0.87;
Matches 86; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1 CGTCCGCGCGCGGCGACTTCGCTTTTCGTCCTCCGCGTACGCGTCCGCGCTCCNNTGAGC 60
DB 105 CGCGCGCGCGCGCGGCGCTCGGCTTGTGGGCTGCGCGAGCTCGCGCTCCNNTGAGC 164
QY 61 GTGCGGCTACCGCGCGCGGCGAGGCGAGGCGGTGGTGGCGATGGCGTGGCTGATGCG 120
DB 165 GAGCTGGGCTGGGCTACGCTCGGATGAGACCGTGTTCGCGTACTGCGCAGCGCG 224
QY 121 CGTTGCGGCGATCGNCTCTNCAATCCNGGTNATNCCGACTTNCNCAAGCCAGGATN 180
DB 225 TCGAGGCGGCGCATCCGACATACGACCTGCGGCTTCGCGCGCTCGCGCAGCGAGCGC 284
QY 181 ATG 183
DB 285 GTG 287

RESULT 10
US-08-777-143-30
; Sequence 30, Application US/08777143
; Patent No. 5843914
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESS: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,143
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-143-30

Query Match          7.8%; Score 34.4; DB 2; Length 419;
Best Local Similarity 47.0%; Pred. No. 0.87;
Matches 86; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1 CGTCCGCGCGCGGCGACTTCGCTTTTCGTCCTCCGCGTACGCGTCCGCGCTCCNNTGAGC 60
```

```
DB 105 CGCGCGCGCGCGGCGGCTCGGCTTGTGGGCTCGCGAGCTCGAGGTGCGCGTGAGC 164
QY 61 GTGCGGCTACCGCGCGCGGCGAGGCGAGGCGGTGGTGGCGATGGCGTGGCTGATGCG 120
DB 165 GAGCTGGGCTGGGCTACGCTCGGATGAGACCGTGTTCGCGTACTGCGCAGCGCG 224
QY 121 CGTTGCGGCGATCGNCTCTNCAATCCNGGTNATNCCGACTTNCNCAAGCCAGGATN 180
DB 225 TCGAGGCGGCGCATCCGACATACGACCTGCGGCTTCGCGCGCTCGCGCAGCGAGCGC 284
QY 181 ATG 183
DB 285 GTG 287

RESULT 11
US-08-775-414-30
; Sequence 30, Application US/08775414
; Patent No. 6090778
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESS: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,414
; FILING DATE: 31-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965805
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-775-414-30

Query Match          7.8%; Score 34.4; DB 3; Length 419;
Best Local Similarity 47.0%; Pred. No. 0.87;
Matches 86; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1 CGTCCGCGCGCGGCGACTTCGCTTTTCGTCCTCCGCGTACGCGTCCGCGCTCCNNTGAGC 60
DB 105 CGCGCGCGCGCGGCGGCTCGGCTTGTGGGCTCGCGAGCTCGAGGTGCGCGTGAGC 164
QY 61 GTGCGGCTACCGCGCGCGGCGAGGCGAGGCGGTGGTGGCGATGGCGTGGCTGATGCG 120
DB 165 GAGCTGGGCTGGGCTACGCTCGGATGAGACCGTGTTCGCGTACTGCGCAGCGCG 224
QY 121 CGCTTGGCGGATCGNCTCTNCAATCCNGGTNATNCCGACTTNCNCAAGCCAGGATN 180
```



Search completed: November 30, 2002, 06:38:44  
Job time : 9078 secs

Search completed: November 30, 2002, 06:38:44  
Job time : 9078 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 03:35:32 ; Search time 34 Seconds  
(without alignments)  
4983.847 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 440  
Sequence: 1 cgtcgcgcgcgcgcacttc.....ggaatnntagataaaaaant 440

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues  
Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118.8	27.0	216	10	US-09-923-876-28
2	63.8	14.5	945	10	US-09-770-445-347
3	57.6	13.1	272	10	US-09-878-574-13031
4	41.4	8.4	269	10	US-09-878-574-6826
5	35	8.0	888	9	US-09-712-363-28
6	35	8.0	888	10	US-09-726-397A-4
7	35	8.0	2209	10	US-09-726-397A-2
8	34.2	7.8	1176	10	US-09-815-242-7814
9	33.6	7.6	460	10	US-09-983-965-278
10	33.6	7.6	465	10	US-09-983-965-71
11	33.4	7.6	491	10	US-09-783-590-1239
12	33.4	7.6	3919	10	US-09-942-366-4
13	33.2	7.5	2467	12	US-10-096-241-1
14	33.2	7.5	5830	10	US-09-070-927A-281
15	33.2	7.5	41936	10	US-09-967-768A-116
16	33.2	7.5	88421	9	US-09-976-059-11
17	33	7.5	2268	12	US-10-096-241-31
18	32.8	7.5	762	10	US-09-815-242-7745
19	32.8	7.5	1140	10	US-09-764-853-362

20	32.8	7.5	2092	10	US-09-764-853-163	Sequence 163, App
21	32.6	7.4	400	10	US-09-925-302-368	Sequence 368, App
22	32.6	7.4	489	10	US-09-974-300-596	Sequence 396, App
23	32.6	7.4	1135	10	US-09-870-162A-12	Sequence 12, Appl
24	32.6	7.4	1164	10	US-09-974-300-260	Sequence 260, App
25	32.6	7.4	14272	10	US-09-870-162A-23	Sequence 23, Appl
26	32.4	7.4	1086	10	US-09-964-824A-4	Sequence 4, Appl
27	32.4	7.4	1086	10	US-09-962-832-141	Sequence 141, App
28	32.4	7.4	7011	10	US-09-954-456-964	Sequence 964, App
29	32.2	7.3	354	10	US-09-978-273-4	Sequence 4, Appl
30	32.2	7.3	750	10	US-09-978-273-2	Sequence 2, Appl
31	32.2	7.3	909	10	US-09-978-273-1	Sequence 1, Appl
32	32.2	7.3	927	10	US-09-815-242-7757	Sequence 7757, Ap
33	32.2	7.3	1267	10	US-09-796-766-19	Sequence 19, Appl
34	32.2	7.3	2324	10	US-09-923-876-1677	Sequence 1677, App
35	32	7.3	252	10	US-09-815-242-7883	Sequence 7883, Ap
36	32	7.3	819	10	US-09-147-346-1	Sequence 1, Appl
37	32	7.3	1152	10	US-09-480-236-2	Sequence 2, Appl
38	32	7.3	1803	10	US-09-147-346-3	Sequence 3, Appl
39	32	7.3	1889	10	US-09-452-599-20	Sequence 20, Appl
40	32	7.3	2760	10	US-09-923-876-850	Sequence 850, App
41	31.8	7.2	236	10	US-09-294-093B-798	Sequence 798, App
42	31.8	7.2	278	10	US-09-764-864-651	Sequence 651, App
43	31.8	7.2	655	10	US-09-764-864-221	Sequence 221, App
44	31.8	7.2	1245	10	US-09-887-576-820	Sequence 820, App
45	31.8	7.2	1479	10		

## ALIGNMENTS

## RESULT 1

US-09-923-876-28  
; Sequence 28, Application US/09923876  
; Patent No. US20020013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Kamigaki, Laura V. (Ito)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 28  
; LENGTH: 216  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700142447H1  
US-09-923-876-28

Query Match 27.0%; Score 118.8; DB 10; Length 216;  
Best Local Similarity 86.5%; Pred No. 2.7e-27;  
Matches 134; Conservative 0; Mismatches 20; Indels 1; Gaps 1;  
QY 82 CCAGGGCAGCGGTGTGGCGATGCGTTCGATGCGCGCTTGGGGNGATCGNCTCC 141  
Db 1 CAAGGGCAGCGGTGTGGCGATGCGTTCGCGCTTGGGGNGATCGCGCTCC 60  
QY 142 TNCATCGNGTATNCCCGACATTCACAAAGCCAGGAGATNATGTTTCAGGACATCANGANG 201  
Db 61 TCCATCGCGGTATCCCGGACTTCCCAAGCCAGGAGATCATGTTCCAGGACATCAGCAG 120  
QY 202 NTGNTGTTCATCCCAAGCGGNTCGTGACACAT 236  
Db 121 TTG-TGTCGATCCCAAGSGCTTCGTTGACACAT 154

```
RESULT 2
US-09-770-445-347
; Sequence 347, Application US/09770445
; Patent No. US2002023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthews, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Sladger, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 203US (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(945)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-347

Query Match 14.5%; Score 63.8; DB 10; Length 945;
Best Local Similarity 61.4%; Pred. No. 5.3e-10;
Matches 89; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 136 GNCCTCTNCATCCNGTATCCCGACTTNCACAAAGCCGAGGATGATGTTTCAGGACATC 195
      ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 2 GCCTCTTCCATTAGATCATCCCGACTTCCCTAAACCCAGGAATCATGTTTCAGGACATA 61

QY 196 ANGANGNTGNTGTTGATCCCAAGGCGTCCGTCACAAATATACCATTTTGTCAAGCGG 255
      ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 62 ACGAGCGTCTCTCGACACTGAGCGCTTAAGGATACATCTGTTGTTGTTGCATAGA 121

QY 256 TACAAGGACCAAGGATACACCTGG 280
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 122 TACAAGATTAAGGCATATCTGTTG 146

RESULT 3
US-09-878-574-13031
; Sequence 13031, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B

Query Match 9.4%; Score 41.4; DB 10; Length 269;
Best Local Similarity 52.8%; Pred. No. 0.002;
Matches 121; Conservative 0; Mismatches 104; Indels 4; Gaps 3;

QY 209 TCGATPCCCAAGGCGTCCGTCGACACATATACCATTTTGTCAAGCGGTACAGGACCAAG 268
      ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 1 TTGATACAAAGGCTTTTCAAGACACACCGTTGACTTGTGTTGTGAGAGGTACAGATCAAA 60

QY 269 GNATCACCNTGGAAANTAGGAGTTAAAGCTAGAGGGTNCATTTTCGGAACAACCTANNCT 328
      ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 61 ACATCAATGTG-TCCGAGGAGTTGAAGCAAGGGCGCTTTATTTGTTCCACCCATTGC- 118

QY 329 TANAANNAATTTGGTCAAAATNGCTGNCNATTTGAGGAAGCNAATNAGTGCACGACNA 388
      ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 119 -ATTAGCTATTGGAGCAAAATTTGTCCCA-TGAGGAACCCCAATAATTCCTTGGGGAG 176

QY 389 ATGATTTTNGAATFANGAATTTTNGGAATNNGGAATNNTAGATAAAA 437
      ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 177 GTTATCTCAGAGAGATTCTTTTGGAGTATGGAACACAGCAAAATGAGA 225

RESULT 5
US-09-712-363-28
; Sequence 28, Application US/09712363
; Patent No. US20020164588A1
```



GENERAL INFORMATION:  
APPLICANT: Eisenberg, David  
APPLICANT: Rotstein, Sergio H.  
APPLICANT: Marcotte, Edward M.  
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND  
INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS  
FILE REFERENCE: 07419-032001  
CURRENT APPLICATION NUMBER: US/09/712,363  
CURRENT FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: PCT/US00/02246  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/119,531  
PRIOR FILING DATE: 2000-02-01  
PRIOR APPLICATION NUMBER: 60/117,844  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/118,206,  
PRIOR FILING DATE: 1999-02-01  
PRIOR APPLICATION NUMBER: 60/126,593  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/134,093  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/134,092  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/165,124  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/165,086  
PRIOR FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 292  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 888  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
US-09-712-363-28

Query Match 8.0%; Score 35; DB 9; Length 888;  
Best Local Similarity 47.1%; Pred. No. 0.38;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 43 GTCCGGCTCCNNTGAGCGTGCCTCACCGCGGCGAGGCGGCGGTGTGGCG 102  
DB 106 GTGGCGGAGCGGATGCCGATCGGCCCACTACCTGGCGCAGACCTATTTCGGTGTGGTG 165  
QY 103 ATGGCGTNCGCTGATCGCGCTTGCGGNGATCGNCTCTNCAATCCNGGTNATNCCGAC 162  
DB 166 AGCTCGGCGCGGCGGCGGAGAACGCGGTCGTCGTCGCGGTCAACACGACC 225  
QY 163 TTNCCAAGCCAGGATNATGTTTCAGGACATCANGANGTNGTGTGA 212  
DB 226 GACGTCGAGCGGTGATCGCGATCTGCCGACGCGACTGCGGCGGCCGA 275

RESULT 6  
US-09-726-397A-4  
Sequence 4, Application US/09726397A  
Patent No. US20020142011A1  
GENERAL INFORMATION:  
APPLICANT: PARISH, TANYA  
APPLICANT: SMITH, DEBBIE  
TITLE OF INVENTION: VACCINE  
FILE REFERENCE: 117-329  
CURRENT APPLICATION NUMBER: US/09/726,397A  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 0014845.20  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 888  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
US-09-726-397A-4

Query Match 8.0%; Score 35; DB 10; Length 888;  
Best Local Similarity 47.1%; Pred. No. 0.38;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 43 GTCCGGCTCCNNTGAGCGTGCCTCACCGCGGCGAGGCGGCGGTGTGGCG 102  
DB 106 GTGGCGGAGCGGATGCCGATCGGCCCACTACCTGGCGCAGACCTATTTCGGTGTGGTG 165  
QY 103 ATGGCGTNCGCTGATCGCGCTTGCGGNGATCGNCTCTNCAATCCNGGTNATNCCGAC 162  
DB 166 AGCTCGGCGCGGCGGCGGAGAACGCGGTCGTCGTCGCGGTCAACACGACC 225  
QY 163 TTNCCAAGCCAGGATNATGTTTCAGGACATCANGANGTNGTGTGA 212  
DB 226 GACGTCGAGCGGTGATCGCGATCTGCCGACGCGACTGCGGCGGCCGA 275

RESULT 7  
US-09-726-397A-2  
Sequence 2, Application US/09726397A  
Patent No. US20020142011A1  
GENERAL INFORMATION:  
APPLICANT: PARISH, TANYA  
APPLICANT: SMITH, DEBBIE  
TITLE OF INVENTION: VACCINE  
FILE REFERENCE: 117-329  
CURRENT APPLICATION NUMBER: US/09/726,397A  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 0014845.20  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 2209  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (434)...(439)  
OTHER INFORMATION: unknown  
NAME/KEY: misc\_feature  
LOCATION: (452)...(704)  
OTHER INFORMATION: unknown  
US-09-726-397A-2

Query Match 8.0%; Score 35; DB 10; Length 2209;  
Best Local Similarity 47.1%; Pred. No. 0.64;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 43 GTCCGGCTCCNNTGAGCGTGCCTCACCGCGGCGAGGCGGCGGTGTGGCG 102  
DB 106 GTGGCGGAGCGGATGCCGATCGGCCCACTACCTGGCGCAGACCTATTTCGGTGTGGTG 165  
QY 103 ATGGCGTNCGCTGATCGCGCTTGCGGNGATCGNCTCTNCAATCCNGGTNATNCCGAC 162  
DB 166 AGCTCGGCGCGGCGGAGAACGCGGTCGTCGTCGCGGTCAACACGACC 225  
QY 163 TTNCCAAGCCAGGATNATGTTTCAGGACATCANGANGTNGTGTGA 212  
DB 226 GACGTCGAGCGGTGATCGCGATCTGCCGACGCGACTGCGGCGGCCGA 275

RESULT 8  
US-09-815-242-7814  
Sequence 7814, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.

```

; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7814
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1176)
US-09-815-242-7814

Query Match
Best Local Similarity 7.8%; Score 34.2; DB 10; Length 1176;
Matches 87; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 32 CCGCGTCAGCGTGGCGTCCNTGAGTGGCGTCCAGCGGCGGAGGCGAGG 91
DB 980 CCTGACACCTCGGCGTACCTGCGGCTGGCGGCTGGCGGCTGGCGGCTGG 1039
QY 92 CGGTGGCGGCGTGGCGTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGG 151
DB 1040 TGGTGGCGGCGTGGCGTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGG 1099
QY 152 TNNATCCGACTNCCAGCGGATNATGTTTCAGGACATCANGATGTTGTCG 211
DB 1100 CGCTGGCGTGGCGTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTG 1159
QY 212 ATCCCAAGGC 221
DB 1160 GTCCCGCTGC 1169

RESULT 9
US-09-983-965-278/c
; Sequence 278, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 278
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 09-BOVMS1-007-Q1-E1-C9
US-09-983-965-71

Query Match
Best Local Similarity 7.6%; Score 33.6; DB 10; Length 455;
Matches 93; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 218 AGCGGNTCCGTGACACATATACCATTTTGTCAAGCGGTACAGGACCAAGGNATCCCN 277
DB 444 AGTTGAAACCTGAAATTTCCACCATTTCTAGTTAAACAAATGAGTAGCATGGAACATAA 385
QY 278 TGGAAANTAGAGGTGTTAAAGCTAGAGGNTCANTTTCCGGAACAACACTANNCTTANAANAA 337
DB 384 AAATCTACACCATGCTAACTTAGCAGACTTTATTTTCAGAAAAAATCTCTTTTGGGAAGA 325
QY 338 TTGGTCAAAAAATGTCGNCNATTTGAGGACGNNATNAGTCCANGCNAATCATTTTN 397
DB 324 TAACTCAAAAATGTTTAAATTAATTTATTTATTTTAAAAATACATTTCTTATTC 265
QY 398 ANCAATGAAATTTTNGGATNNGGATNNGGATNNGGATNNGGATNNGGATNNGGAT 437

; LENGTH: 460
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 34-BOVMS1-006-Q1-E1-A6
US-09-983-965-278

Query Match
Best Local Similarity 7.6%; Score 33.6; DB 10; Length 450;
Matches 84; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 243 TTTTGTCAAGCGGTACAGGACCAAGNATCCACCTTGGAAANTAGGATTTAAAGCTAGAG 302
DB 208 TCTAGTTAAACAAATGAGTAGCAGCACTAAAAAAATCTACACCTGCTAGGTTAGCA 149
QY 303 GGWCTANTTTCGGAACAACACTANNCTTTANAANNAATTTGGTCAAAAATNGTGCNATGGA 362
DB 148 GACTTTATTTTCAGAAAAATGCTTTTGGGAAGAATAACTCAAAAAATGTTTTAAATAAA 89
QY 363 GGAAGCNAATNAGTGCACGCAAAATGATTTTNGAATANGAATTTTNGGAATNNGG 422
DB 88 TTTATTTATTTTAAAAATACAAATGCTATTCACATCTATGTTTATTTGCTCATCTAGG 29
QY 423 AATNNTAGATAAAAA 437
DB 28 TAACCTTGAGAAAAA 14

RESULT 10
US-09-983-965-71/c
; Sequence 71, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 71
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 09-BOVMS1-007-Q1-E1-C9
US-09-983-965-71
```



Query Match 7.6% Score 33.4; DB 10; Length 3919;  
Best Local Similarity 48.7%; Pred. No. 2.8;  
Matches 76; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 6 GCGCGCGCGGACCTTCCTTCCTCCCGCTCAGCGCTCGCGGCTCCNNTGAGCGTGGC 65  
DB 129 GTGACAGCGGATTCATCTCTCGAGCTGCGCGCGGCTTTGGGCTCAGCGCGCGG 188  
QY 66 CTTACACCGCGGCGGAGCGGAGCGGTGTGGCGATGGGCTGCTGATCGCGGCTT 125  
DB 189 GCTCCGCTCGCGCGGAGTCTTCGAGCGAGCGGAGCGCGCGCGGAGTCCGAGCTC 248  
QY 126 GCGGNGATCGCTCTTCATCTCCNGTGTATNCCGA 161  
DB 249 TGGTGGCAGCTGAGCGCGCGCGCGCGCTCGCGCA 284

RESULT 13  
US-10-096-241-1/c  
; Sequence 1, Application US/10096241  
; Patent No. US20020127594A1  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; Busfield, Samantha J.  
; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES  
; AND USES THEREFOR  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/096,241  
; FILING DATE: 12-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/699,591  
; FILING DATE: 19-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fasse, J. Peter  
; REGISTRATION NUMBER: 32,983  
; REFERENCE/DOCKET NUMBER: 07334/022001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2467 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 79..1893  
; OTHER INFORMATION:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-096-241-1

Query Match 7.5% Score 33.2; DB 12; Length 2467;  
Best Local Similarity 59.6%; Pred. No. 2.4; 36; Indels 0; Gaps 0;  
Matches 53; Conservative 0; Mismatches 36;

QY 36 CGTCAGCGCTCGCGCTCCNNTGAGCGTGGCGCTCACCAGCGGCGGAGGCGAGCGGT 95  
DB 1574 CGCCAGCGCGCGCGCGCGCGCGCTCTCTCGGAGCGCGCGCGCTCGCGCGCGCG 1515  
QY 96 GTGGCGGAGCGCTGCTGATGCGCGCT 124  
DB 1514 GCGCGCGGCGCGCGCGCTCTCTCGGTGT 1486

RESULT 14  
US-09-070-927A-281  
; Sequence 281, Application US/09070927A  
; Patent No. US20020120116A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Kunsch  
; Steven Barash  
; Patrick J. Dillon  
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 982  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,927A  
; FILING DATE: 04-May-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,655  
; FILING DATE: 1997-05-16  
; APPLICATION NUMBER: 60/044,031  
; FILING DATE: 1997-05-06  
; APPLICATION NUMBER: 60/066,009  
; FILING DATE: 1997-11-14  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kealey K. Hoover  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PB369  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 281:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5830 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 281:  
US-09-070-927A-281

Query Match 7.5% Score 33.2; DB 10; Length 5830;  
Best Local Similarity 46.8%; Pred. No. 4;  
Matches 94; Conservative 1; Mismatches 105; Indels 1; Gaps 1;

QY 142 TNCATCCNGGTATNCCGACTTNCAGAGCGGATGATGTTTCAGGACATCANGANG 201  
DB 5037 TACATTGAAGCATTCAGATTATCTCTGAGAAAGGATCGTGTTCGTGACATVCTCCA 5096  
QY 202 NTGNTGTTCGATCCAGCGGNTCCGTGCAACATATACCATTTTGTCAAGCGGTACAG 261  
DB 5097 TTAATGGCTATGGGATGCTATCTGTGAGCAAGCAACAATCTGGATTACGGGAA 5156  
QY 262 GACCAAGATACACCTGTAAGTAAAGCTAGAGGNTCAANTTTTCGGAACAC 321  
DB 5157 GAAAAAGATGATATG-TTGTAGGACCGGAAGCTCGTGGCTTTATTGTCGGCTGCC 5215

```

QY      322  TANNCTTANNNATTCGT 342
      |||||
Db      5216  AGTGGCTTATGAAGTGGGT 5236

RESULT 15
US-09-967-768A-116
; Sequence 116, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 41936
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-116

Query Match      7.5%; Score 33.2; DB 10; Length 41936;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY      35  CGGTACGGCTCGCGGCTCCNNATGAGCGTGCACGGCGGCGAGCGGCGAGCGGCGG 94
      |||||
Db      17753  CGGCGCGCGCGCGCTGTCGGCGGAGCGCTTGGCGGCGCCCGGAGCGGCGGCGGCGGCGG 17812

QY      95  TGGTGGCGATGCGGTTCGCTGTATGATCGCGCTTGGCGGNG 132
      |||||
Db      17813  AGCGGCGCGCGCTGTCACGCGCTGCAGGAGCGCGCGGCG 17850

Search completed: November 30, 2002. 04:09:42
Job time : 63 secs

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 04:01:22 ; Search time 71 Seconds  
(without alignments)

4194,548 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtccgcgcgcgcgcacttc.....ggaaatnntagataaaaaant 440

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 344316 seqs, 338423730 residues

Total number of hits satisfying chosen parameters: 688632

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/prodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.2	9.1	18477	1	PCT-US02-32727-129
2	35	8.0	1431	5	US-09-724-676-40760
3	35	8.0	1431	5	US-09-724-676A-40760
4	35	8.0	1634	5	US-09-724-676-40759
5	35	8.0	1634	5	US-09-724-676A-40759
6	35	8.0	2137	5	US-09-724-676-40758
7	35	8.0	2137	5	US-09-724-676A-40758
8	34	7.7	2259	5	US-09-724-676-13643
9	34	7.7	2259	5	US-09-724-676A-13643
10	34	7.7	2299	5	US-09-724-676-13641
11	34	7.7	2299	5	US-09-724-676A-13641
12	34	7.7	2318	5	US-09-724-676-13645
13	34	7.7	2318	5	US-09-724-676A-13645
14	34	7.7	2353	5	US-09-724-676-13642
15	34	7.7	2353	5	US-09-724-676A-13642
16	34	7.7	2358	5	US-09-724-676-13640
17	34	7.7	2358	5	US-09-724-676A-13640
18	34	7.7	2412	5	US-09-724-676-13644
19	34	7.7	2412	5	US-09-724-676A-13644
20	33.4	7.6	9922	1	PCT-US02-32727-89
C 21	33.2	7.5	1921	5	US-09-724-676-40762
C 22	33.2	7.5	1921	5	US-09-724-676A-40762
C 23	33.2	7.5	2124	5	US-09-724-676-40761
C 24	33.2	7.5	2124	5	US-09-724-676A-40761
C 25	33.2	7.5	2137	5	US-09-724-676-40758
C 26	33.2	7.5	2137	5	US-09-724-676A-40758

C 27 33.2 7.5 4044 5 US-09-724-676-40755 Sequence 40755, A  
C 28 33.2 7.5 4044 5 US-09-724-676A-40755 Sequence 40755, A  
C 29 33 7.5 916 5 US-09-724-676-14375 Sequence 14375, A  
C 30 33 7.5 916 5 US-09-724-676A-14375 Sequence 14375, A  
C 31 33 7.5 1078 5 US-09-724-676-14374 Sequence 14374, A  
C 32 33 7.5 1078 5 US-09-724-676A-14374 Sequence 14374, A  
C 33 33 7.5 1995 5 US-09-724-676-14377 Sequence 14377, A  
C 34 33 7.5 1995 5 US-09-724-676A-14377 Sequence 14377, A  
C 35 33 7.5 2157 5 US-09-724-676-14376 Sequence 14376, A  
C 36 33 7.5 2157 5 US-09-724-676A-14376 Sequence 14376, A  
C 37 33 7.5 2858 5 US-09-724-676-14372 Sequence 14372, A  
C 38 33 7.5 2858 5 US-09-724-676A-14372 Sequence 14372, A  
C 39 32.6 7.4 2053 5 US-09-724-676-20591 Sequence 20591, A  
C 40 32.6 7.4 2053 5 US-09-724-676A-20591 Sequence 20591, A  
C 41 32.4 7.4 852 5 US-09-724-676-31241 Sequence 31241, A  
C 42 32.4 7.4 852 5 US-09-724-676A-31241 Sequence 31241, A  
C 43 32.4 7.4 2089 5 US-09-724-676-31239 Sequence 31239, A  
C 44 32.4 7.4 2089 5 US-09-724-676A-31239 Sequence 31239, A  
C 45 32.4 7.4 2114 5 US-09-724-676-31240 Sequence 31240, A

## ALIGNMENTS

RESULT 1  
PCT-US02-32727-129  
; Sequence 129, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Jannli  
; APPLICANT: Wang, Siqing  
; APPLICANT: Jen, Shylan  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30952  
; SEQ ID NO 129  
; LENGTH: 18477  
; TYPE: DNA  
; ORGANISM: propioni acnes  
PCT-US02-32727-129

Query Match 9.1%; Score 40.2; DB 1; Length 18477;  
Best Local Similarity 61.4%; Pred. No. 0.15;  
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
QY 133 ATCCGCTCTTCATCCNGGTATCCCGACTTCCCAAGAGCCAGGATGTTTCAGGAC 192  
DB 8406 ATTGCCAGCTGATCCGGGATGTCCTCGGACTTCCCGAGCCCGGGTCACTTTTAAGGAC 8465  
QY 193 ATCCAGANGNTGNTGTCATCCCAAGG 220  
DB 8466 ATCACTCCGCTACTGGCAATCCCAATG 8493

RESULT 2  
US-09-724-676-40760  
; Sequence 40760, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: CompuGen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 CompuGen

	Query Match	8.0%	Score 35;	DB 5;	Length 1431;
	Best Local Similarity	53.5%;	Pred. No. 1.3;		
	Matches	68;	Conservative	0; Mismatches	59; Indels
				0; Gaps	0;
QY	6	GCGCCGCCGACATTCGCCTTTTGTGCCCCCGGTCAAGCTCCCGCTCCNNNTGACGGTGCG	65		
DB	442	GAGGAGGACGACATGACATCCTGCTGGCCCCGCTGTGGGGGTCCCGCGCGCCCCG	501		
QY	66	CCTCACCGCGGCGGCGAGGCGGTGGTGGCATGCGCTTNCGTGTATGCGCGCTT	125		
DB	502	GGCCCGCGCCC CGCGCGGGGCGAGGAGCCGTTGGGGCGCGGCGCGCGCGCGCG	561		
QY	126	GGCGNG	132		

```

RESULT 5
US-09-724-676A-40759
,, Sequence 40759; Application US/09724676A
,, GENERAL INFORMATION:
,, APPLICANT: Compugen LTD
,, TITLE OF INVENTION: Variants of alternative splicing
,, FILE REFERENCE: 129181.4 Compugen
,, CURRENT APPLICATION NUMBER: US/09/724,676A
,, CURRENT FILING DATE: 2000-11-28
,, NUMBER OF SEQ ID NOS: 97222
,, SOFTWARE: PatentIn version 3.2
,, SEQ ID NO 40759
,, LENGTH: 1634
,, TYPE: DNA
,, ORGANISM: Homo sapiens
,, FEATURE:
,, NAME/KEY: misc.feature
,, LOCATION: (31)..(31)
,, OTHER INFORMATION: n is a,c,g, or t
,, FEATURE:
,, NAME/KEY: misc.feature
,, LOCATION: (48)..(48)
,, OTHER INFORMATION: n is a,c,g, or t
US-09-724-676A-40759

```





[illegible]

Db	438	CGTCGGGAGCGGGGCGCCGCGAGGCCCCCGCGCGGCGCGCGGCGCGAGGACCTGCG	497
Oy	66	CGTACCGGCGCAGGCGAGGCGAGCGGCGTGGCGATGGGCTNCGCTGATGGCGCGTT	125
Db	498	CCGAGCGCTGCCCGCCCGAATGCGCGCGCGCGAGCCGGGCTCCCGGCGCGGCGCCTA	557
Oy	126	GGCGG	130
Db	558	GGCGG	562

Search completed: November 30, 2002, 04:11:06  
Job time : 92 secs

QY 126 GGCG 130  
DB 558 GGCG 562

```

RESULT 14
US-09-724-676-13642
: Sequence 13642, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Comugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 CompuGen
: CURRENT APPLICATION NUMBER: US/09/724,676
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 13642
: LENGTH: 2353
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-724-676-13642

Query Match      7.7%  Score 34;  DB 5;  Length 2353;
Best Local Similarity 53.6%  P-Val 0.34;
Matches 67;  Conservative
Mismatches 58;  Indels 0;  Gaps 0;

```

```

RESULT 15
US-09-724-676A-13642
; Sequence 13642, Application US/09724676A
; GENERAL INFORMATION:
; TITLE: 3D-CPUGEN: LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 139131.4
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13642
; LENGTH: 2353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-13642

Query Match      7.7%;      Score 34; DB 5; Length 2353;
Matches Local Similarity 53.6%;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```

Qy	5	CGCCCGCGCGACTTCGCTCTTTTGTCTCCCGCGCTAGCGTGCCTCCNNTGAGCGTCGC	65
Db	438	CGCTCGGGAGCGGGCGCCCGAGGCCCCCGCGGGGCGCGGCGCAGGAGACCTGCG	497
Qy	66	CGTCACCGCGCGAGCGAGGCGAGCGGTGGTGCGCATGCGCTNGCTGATGCGCGCTT	125
Db	498	CCGCGAGCGCTGCCCGCCGAAATGGCGCGCGCGCGAGCGGGCTCCCGCGCGCGGCCCTA	557

